

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:10:57 ; Search time 50.3556 Seconds
(without alignments)
740.659 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	692	100.0	132	5	ABG76923	Abg76923 Mouse 3D6
2	650	93.9	135	5	ABB79729	Abb79729 Anti-Stre
3	644	93.1	239	6	ABP58274	Abp58274 Humanised
4	641	92.6	132	2	AAR12361	Aar12361 Light (ka
5	640	92.5	132	5	ABG76925	Abg76925 Humanised
6	639	92.3	131	2	AAR12239	Aar12239 Mouse MAb
7	636	91.9	132	6	ABG74244	Abg74244 Mouse ant
8	630	91.0	132	5	ABG76931	Abg76931 Humanised
9	628	90.8	132	2	AAR24712	Aar24712 Sequence

10	606	87.6	142	4	AAE07032	Aae07032 Murine an
11	595	86.0	239	2	AAR24811	Aar24811 Sequence
12	589	85.1	239	7	ADD47025	Add47025 Rat Prote
13	571	82.5	113	4	AAE03751	Aae03751 Murine PS
14	571	82.5	218	4	AAE03756	Aae03756 Chimeric
15	562	81.2	353	2	AAAY06273	Aay06273 Anti Fc a
16	560	80.9	112	4	AAE06946	Aae06946 Murine 1D
17	560	80.9	112	4	AAU09918	Aau09918 Murine mA
18	560	80.9	112	5	ABG75527	Abg75527 Mouse mAb
19	560	80.9	112	7	ABR61865	Abr61865 Mouse MAb
20	560	80.9	257	3	AAB09777	Aab09777 Antiviral
21	559	80.8	112	2	AAAY52765	Aay52765 Anti-tiss
22	559	80.8	112	2	AAAY52766	Aay52766 Anti-tiss
23	556	80.3	112	4	AAE06991	Aae06991 Human kap
24	555	80.2	112	5	AAO14971	Aao14971 Mouse lig
25	550	79.5	243	2	AAW60769	Aaw60769 Single ch
26	548	79.2	112	2	AAW48248	Aaw48248 A77 anti-
27	548	79.2	112	4	AAB74621	Aab74621 A77 anti-
28	548	79.2	112	4	AAE08554	Aae08554 Murine A7
29	548	79.2	535	2	AAW28491	Aaw28491 Human p53
30	548	79.2	535	2	AAW28492	Aaw28492 Human p53
31	547	79.0	162	7	ADE06760	Ade06760 D13 light
32	546	78.9	112	7	ABR62960	Abr62960 Monoclonal
33	543	78.5	113	6	ABP58270	Abp58270 Humanised
34	543	78.5	219	6	ABP58272	Abp58272 Humanised
35	539	77.9	272	2	AAW43913	Aaw43913 Mus muscu
36	538	77.7	112	4	AAE06951	Aae06951 Humanised
37	538	77.7	112	4	AAU09923	Aau09923 Humanised
38	538	77.7	112	5	ABG75532	Abg75532 Humanised
39	538	77.7	112	6	ABB99636	Abb99636 2A2 monoc
40	537	77.6	132	2	AAW79225	Aaw79225 Humanised
41	537	77.6	132	2	AAW56349	Aaw56349 Humanised
42	537	77.6	132	2	AAAY30186	Aay30186 Sequence
43	536	77.5	113	7	ADD05270	Add05270 Female mo
44	535	77.3	272	2	AAW00557	Aaw00557 Nematode
45	533	77.0	112	4	AAE06952	Aae06952 Humanised

ALIGNMENTS

RESULT 1

ABG76923

ID ABG76923 standard; protein; 132 AA.

XX

AC ABG76923;

XX

DT 05-NOV-2002 (first entry)

XX

DE Mouse 3D6 VL protein.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX
 OS Mus musculus.
 XX
 PN WO200246237-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-US046587.
 XX
 PR 06-DEC-2000; 2000US-0251892P.
 XX
 PA (NEUR-) NEURALAB LTD.
 PA (AMHP) WYETH.
 XX
 PI Basi G, Saldanha J, Yednock T;
 XX
 DR WPI; 2002-519658/55.
 DR N-PSDB; ABS59426.
 XX
 PT Novel light/heavy chain of humanized immunoglobulin for treating
 PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
 PT determining regions and variable framework region from human acceptor
 PT immunoglobulin.
 XX
 PS Claim 67; Fig 1; 171pp; English.
 XX
 CC The present invention relates to new humanized immunoglobulin (Ig) light
 CC chain (LC) or heavy chain (HC) comprising variable region complementarity
 CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
 CC and variable framework region from human acceptor Ig LC or HC sequence.
 CC The invention is useful for preventing or treating an amyloidogenic
 CC disease or Alzheimer's disease in a patient. The invention is also useful
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
 CC variable heavy (VH) chain protein of the invention
 XX
 SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.7e-55;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLVLWIRETNGYVVM	QTPLT	LSVTIGQPASISCKSSQSLLDSDGKTYLNW	60	
Db	1	MMSPAQFLFLVLWIRETNGYVVM	QTPLT	LSVTIGQPASISCKSSQSLLDSDGKTYLNW	60	
Qy	61	LLQRPQGSPKR	LIYLVSKLDSGVPDRFTGSGSGTDFTLKISR	IEAEDLGLYYCWQGTHFP	120	
Db	61	LLQRPQGSPKR	LIYLVSKLDSGVPDRFTGSGSGTDFTLKISR	IEAEDLGLYYCWQGTHFP	120	
Qy	121	RTFGGGTKLEIK				132
Db	121	RTFGGGTKLEIK				132

RESULT 2
 ABB79729

ID ABB79729 standard; protein; 135 AA.
 XX
 AC ABB79729;
 XX
 DT 29-OCT-2002 (first entry)
 XX
 DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.
 XX
 KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
 KW antibody; anticaries; transgenic plant; transgenic animal; caries;
 KW immunotherapy; therapy.
 XX
 OS Mus musculus.
 XX
 PN US2002068066-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 15-JUN-2001; 2001US-00881823.
 XX
 PR 20-AUG-1999; 99US-00378577.
 XX
 PA (SHIW/) SHI W.
 PA (MORR/) MORRISON S L.
 PA (TRIN/) TRINH K.
 PA (WIMS/) WIMS L.
 PA (CHEN/) CHEN L.
 PA (ANDE/) ANDERSON M H.
 XX
 PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
 XX
 DR WPI; 2002-565838/60.
 DR N-PSDB; ABN84610.
 XX
 PT Treatment and prevention of dental caries in mammals, in particular
 PT humans by orally administering genetically engineered or purified
 PT antibodies that bind to surface antigens of carcinogenic organisms.
 XX
 PS Claim 13; Fig 3A; 30pp; English.
 XX
 CC The present sequence is the protein sequence of the light chain variable
 CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds
 CC specifically to the surface antigens of cariogenic type c Streptococcus
 CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
 CC HB 12558) hybridoma cells. In an example from the invention, chimeric
 CC monoclonal antibody TEFEE was produced comprising SWLA3 variable regions
 CC and human antibody constant regions. Such chimeric monoclonal antibodies
 CC can be used to prevent or treat dental caries in humans. The antibodies
 CC engage the effector apparatus of the human immune system when they bind
 CC cariogenic organisms, resulting in their destruction. The chimeric
 CC antibodies may be produced in edible plants, in transgenic animals, or in
 CC chicken eggs for oral ingestion
 XX
 SQ Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;
 Best Local Similarity 93.2%; Pred. No. 3.1e-51;

DT 15-AUG-1991 (first entry)
 XX
 DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
 XX
 KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
 XX
 OS Mus musculus.
 XX
 PN WO9107493-A.
 XX
 PD 30-MAY-1991.
 XX
 PF 13-NOV-1989; 89US-00433730.
 XX
 PR 13-NOV-1989; 89US-00433730.
 XX
 PA (XOMA) XOMA CORP.
 PA (GREC) GREEN CROSS CORP.
 XX
 PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
 XX
 DR WPI; 1991-178105/24.
 DR N-PSDB; AAQ12063.
 XX
 PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
 PT -1 antigen from sample.
 XX
 PS Disclosure; Fig 18; 107pp; English.
 XX
 CC This is the light (kappa) - chain variable (V) region of a mouse
 CC monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral
 CC antigen. It is used in the construction of a chimeric MAb comprising
 CC heavy and light chains having murine V regions and human C regions. The
 CC chimeric MAbs are more effective than murine MAb 4D12 since they have an
 CC increased compatibility in humans. The heavy and light chain V-regions
 CC are joined by manipulating their respective joining (J) regions, to
 CC generate restriction enzyme recognition sites. The chimeric MAbs can be
 CC used as immunoconjugates, in association with e.g. toxins for HIV
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
 CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 132 AA;

Query Match 92.6%; Score 641; DB 2; Length 132;
 Best Local Similarity 90.9%; Pred. No. 2e-50;
 Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 |||
 Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASFCKSSQSLLDSDGKTFLNW 60
 Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 |||
 Db 61 FLQRPGQSPKRLLYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHP 120
 Qy 121 RTFGGGTKLEIK 132

Db ||| |||||::
 121 ITFGAGTKLELR 132

RESULT 5

ABG76925

ID ABG76925 standard; protein; 132 AA.

XX

AC ABG76925;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #1.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;

KW Abeta.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

PT Novel light/heavy chain of humanized immunoglobulin for treating

PT amyloidogenic disease, has 3D6/10D5 variable region complementarity

PT determining regions and variable framework region from human acceptor

PT immunoglobulin.

XX

PS Claim 54; Page 154; 171pp; English.

XX

CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity

CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,

CC and variable framework region from human acceptor Ig LC or HC sequence.

CC The invention is useful for preventing or treating an amyloidogenic

CC disease or Alzheimer's disease in a patient. The invention is also useful

CC for in vivo imaging amyloid deposits in a patient. The present amino acid

CC sequence represents a humanized 3D6 variable light (VL) chain or variable

CC heavy (VH) chain protein of the invention

XX

SQ Sequence 132 AA;

Query Match 92.5%; Score 640; DB 5; Length 132;
Best Local Similarity 90.2%; Pred. No. 2.5e-50;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNW 60

Qy     61 LLQRPQGQSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLTKISRIEAEDLGLYYCWQGTHFP 120
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db     61 LLQKPGQSPQRLIYLVSKLD SGVPDRFSGSGSGTDFTLTKISRVEAEDVGVYYCWQGTHFP 120

Qy    121 RTFGGGTKLEIK 132
          |||| |||:|||
Db    121 RTFGQGTKVEIK 132
```

RESULT 6

AAR12239

ID AAR12239 standard; protein; 131 AA.

XX

AC AAR12239;

XX

DT 25-MAR-2003 (revised)

DT 19-AUG-1991 (first entry)

XX

DE Mouse MAb 4D12 L chain V region.

XX

KW HIV-1; chimera.

XX

OS Mus sp.

XX

PN WO9107494-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00433703.

XX

PR 13-NOV-1989; 89US-00433703.

XX

PA (XOMA) XOMA CORP.

PA (GREC) GREEN CROSS CORP.

PA (ZOMA-) ZOMA CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX

DR WPI; 1991-178106/24.

DR N-PSDB; AAQ12019.

XX

PT New chimeric mouse human antibodies - used in treatment, diagnosis and
PT prophylaxis of HIV infections.

XX

PS Disclosure; Fig 18; 108pp; English.

XX

CC The mouse VL gene product may be used to produce chimeric mouse- human

DR N-PSDB; ABX16570.
 XX
 PT New chimeric molecule useful in treating patients with disorders, such as
 PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
 PT comprises GD3 and/or PSMA binding domains of antibody.
 XX
 PS Disclosure; Page 13; 35pp; English.
 XX
 CC The invention relates to a chimaeric molecule comprising the GD3
 CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
 CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
 CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
 CC sequences, the zeta signalling chain of the T cell receptor and an
 CC intervening CD8alpha hinge in which cysteine residues have been mutated.
 CC The chimaeric molecules expressed in T cells or NK cells or other
 CC effector cells are useful in treating patients with cancers expressing
 CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
 CC and/or together with each other or with heterologous constructs to engage
 CC additional stimulatory and functional properties of the effector cells to
 CC enhance the antitumour therapeutic efficacy (claimed). They are
 CC particularly useful in disorders including melanoma, neuroendocrine
 CC tumours and prostate and small cell lung cancer. The present sequence
 CC represents the mouse antibody 3D8 light chain variable region
 XX
 SQ Sequence 132 AA;

Query Match 91.9%; Score 636; DB 6; Length 132;
 Best Local Similarity 93.9%; Pred. No. 5.7e-50;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWL 61
 |||||:|||||
 Db 1 MSPAQFLFLVLWIQETNGDVVMQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
 Qy 62 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTTHFPR 121
 |||||:|||||
 Db 61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTTHFPH 120
 Qy 122 TFGGGTKLEIK 132
 |||||
 Db 121 TFGGGTKLEIK 131

RESULT 8

ABG76931

ID ABG76931 standard; protein; 132 AA.

XX

AC ABG76931;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #2.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;

KW variable region complementarity determining region; 3D6; 10D5;

KW variable framework region; amyloidogenic disease; Alzheimer's disease;

KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

RESULT 9

AAR24712

ID AAR24712 standard; protein; 132 AA.

XX

AC AAR24712;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;

KW antithrombotic agent; myocardial infarction therapy.

XX

OS Mus musculus.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .20
----	---------	--------

FT		/label= leader
----	--	----------------

FT	Region	21. .43
----	--------	---------

FT		/label= Framework Region (FR) 1
----	--	---------------------------------

FT	Region	44. .59
----	--------	---------

FT		/label= complementarity determining region(CDR)1
----	--	--

FT	Region	60. .74
----	--------	---------

FT		/label= FR-2
----	--	--------------

FT	Region	75. .81
----	--------	---------

FT		/label= CDR-2
----	--	---------------

FT	Region	82. .112
----	--------	----------

FT		/label= FR-3
----	--	--------------

FT	Region	113. .122
----	--------	-----------

FT		/label= CDR-3
----	--	---------------

FT	Region	123. .132
----	--------	-----------

FT		/label= FR-4
----	--	--------------

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX

PR 18-DEC-1990; 90JP-00413829.

PR 11-NOV-1991; 91JP-00294464.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Iwasa S, Tada H, Watanabe T;

XX

DR WPI; 1992-209528/26.

DR N-PSDB; AAQ25665.

XX

PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light

PT and heavy chain variable and constant for treating thrombotic conditions

PT e.g. myocardial infarction.

XX

PS Example; Fig 1; 87pp; English.

XX

CC A genomic DNA library was prepd. from mouse anti-human fibrin specific
CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse
CC JK4-5 gene fragment as a hybridisation probe gave three positive
CC recombinant phage clones. Phage clone KE14 was identified as a clone
CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was
CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a
CC functional VK gene formed by recombination between the VK gene belonging
CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25
CC -MAR-2003 to correct PN field.)

SQ Sequence 132 AA;

```
Query Match          90.8%;  Score 628;  DB 2;  Length 132;
Best Local Similarity 91.7%;  Pred. No. 3e-49;
Matches 121;  Conservative 3;  Mismatches 8;  Indels 0;  Gaps 0;
```

```
Qy      1 MMSPAQLFLLVLWIRETNGYVVMQTPLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60  
       | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db      1 MMSPAQLFLLVLWIRETG DVMAQTPLTLSTIGQPAFISCTSSQSLLDSDGKTYLNW 60  
  
Qy     61 LLQRPGQSPKRLIYLVS KLDSGV PDRFTGS GSGTDFTLKISR IEAEDLGLYYCWQGTHFP 120  
       ||| | | | | | | | | | | | | | : |:| | | | | | | | |  
Db     61 LLQRPGQSPKRLIYLVS KLYSGVP DRFTGS GSGTAFTLKINRVE AEDLG VYYC WQGIHFP 120  
  
Qy    121 RTFGGGTKLEIK 132  
        |||||  
Db    121 YTFGGGTKLEIK 132
```

RESULT 10

AAE07032

ID AAE07032 standard; protein; 142 AA.

XX

AC AAE07032;

XX

DT 16-OCT-2001 (first entry)

XX

DE Murine antibody 1D9 kappa light chain variable region.

XX

KW Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; antibody 1D9 kappa light chain variable region.

XX

OS Mus sp.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .17
----	---------	--------

```
FT                /label= Signal peptide
```

FT	Protein	18.	.142
----	---------	-----	------

```
FT      /note= "Murine mature antibody 1D9 kappa light chain
FT      variable region"
```


Db 7 LLVLWIRETIGDVVMTQTPLTSLVTVGHPASISCKSSQSLLDSDGKTFLNWLLQRPQGSP 66

Qy 70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKL 129
 |||:|||||:|||||

Db 67 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPYTFGGGTKL 126

Qy 130 EIK 132
 |||

Db 127 EIK 129

RESULT 11

AAR24811

ID AAR24811 standard; protein; 239 AA.

XX

AC AAR24811;

XX

DT 25-MAR-2003 (revised)

DT 28-DEC-1992 (first entry)

XX

DE Sequence encoded by the chimeric kappa chain cDNA (lgkv) contained in
 DE pTB1427.

XX

KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
 KW antithrombotic agent; myocardial infarction therapy.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .20
----	---------	--------

FT		/label= leader
----	--	----------------

FT	Region	21. .133
----	--------	----------

FT		/label= V-kappa
----	--	-----------------

FT	Misc-difference	130
----	-----------------	-----

FT		/note= "Alternatively = Glu"
----	--	------------------------------

FT	Region	134. .239
----	--------	-----------

FT		/label= C-kappa
----	--	-----------------

XX

PN EP491351-A2.

XX

PD 24-JUN-1992.

XX

PF 17-DEC-1991; 91EP-00121591.

XX

PR 18-DEC-1990; 90JP-00413829.

PR 11-NOV-1991; 91JP-00294464.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Iwasa S, Tada H, Watanabe T;

XX

DR WPI; 1992-209528/26.

DR N-PSDB; AAQ25691.

XX

PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
 PT and heavy chain variable and constant for treating thrombotic conditions
 PT e.g. myocardial infarction.

XX
 PS Example; Fig 9; 87pp; English.
 XX
 CC Poly(A)+ RNA was prepd. from the anti-fibrin chimeric Ab-producing
 CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa
 CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand
 CC cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An
 CC amplified DNA fragment of about 0.33kb was isolated and used to create a
 CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the
 CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa
 CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)
 CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first
 CC stand synthesis and the 5'mV-kappa and 3'mV-kappa primers for the PCR, an
 CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a
 CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a
 CC primer for first strand synthesis and the 5'S-kappa and 3'L- kappa
 CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v: V-
 CC kappa-FIB) were isolated and and used to construct respectively plasmids
 CC pTB1391, pTB1392, and pTB1393. L-kappa, V- kappa and C-kappa were joined
 CC together to give a plasmid, pTB1427, contg. the whole length of the
 CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 239 AA;

Query Match 86.0%; Score 595; DB 2; Length 239;
 Best Local Similarity 85.6%; Pred. No. 5.7e-46;
 Matches 113; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 ||||| : ||||| ||||| ||||| : ||||| |||||
 Db 1 MMSPAQFLFLLVLWIRETRGDIQLAQTPLTFSVTIGQPAFISCTSSQTLLDSDGKTYLNW 60
 Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 ||||| : ||||| ||||| ||||| : ||||| : ||||| |||||
 Db 61 LLQRPGQSPRRLIYLVSKLYSGVPDRFTGSGSGTAFTLKINRVEAEDLGYYCWQGIHFP 120
 Qy 121 RTFGGGTKLEIK 132
 ||||| ||
 Db 121 YTFGGGTKLVIK 132

RESULT 12

ADD47025

ID ADD47025 standard; protein; 239 AA.

XX

AC ADD47025;

XX

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein L22655, SEQ ID NO 12711.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; L22655.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 239 AA;

Query Match 85.1%; Score 589; DB 7; Length 239;
Best Local Similarity 84.7%; Pred. No. 2e-45;
Matches 111; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWL 61

```

      |||||:|:|:| |||||:| |||||:|:|:|
Db      1 MSPAQFLFLMLWIQETSGDVVMTQTPVSLSVAIGQPASISCKSSQSLVGTNGKTYLNWL 60
Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR 121
      |||||:|:|:| |||||:|:|:| |||||
Db      61 LQRPQGSPKRLIYLVSKLDSGIPDRFSGSGSETDFTLKISRVEADDLGVYYCLQGTHFPL 120
Qy      122 TFGGGTKLEIK 132
      ||| |||||
Db      121 TFGSGTKLEIK 131

```

RESULT 13

AAE03751

ID AAE03751 standard; protein; 113 AA.

XX

AC AAE03751;

XX

DT 07-AUG-2001 (first entry)

XX

DE Murine PSCA Ab light chain variable region domain from clone 6B8.1D7.2B3.

XX

KW Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
 KW light chain variable domain; VL.

XX

OS Mus musculus.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	24. .39
----	--------	---------

FT		/label= CDR1
----	--	--------------

FT		/note= "Complementarity determining region 1"
----	--	---

FT	Region	55. .61
----	--------	---------

FT		/label= CDR2
----	--	--------------

FT		/note= "Complementarity determining region 2"
----	--	---

FT	Region	94. .102
----	--------	----------

FT		/label= CDR3
----	--	--------------

FT		/note= "Complementarity determining region 3"
----	--	---

XX

PN WO200140309-A2.

XX

PD 07-JUN-2001.

XX

PF 27-OCT-2000; 2000WO-US029603.

XX

PR 29-OCT-1999; 99US-0162558P.

PR 16-FEB-2000; 2000US-0182872P.

XX

PA (GETH) GENENTECH INC.

XX

PI Devaux B, Keller G, Koeppen H, Lasky LA;

XX

DR WPI; 2001-389954/41.

XX

PT Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
 PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-
 PT expressing cancer cells in vivo, useful for killing PSCA-expressing

PT cancer cells.
 XX
 PS Claim 22; Fig 12; 112pp; English.
 XX
 CC The present sequence is murine prostate stem cell antigen (PSCA) antibody
 CC (Ab) light chain variable region domain (VL) from hybridoma clone
 CC 6B8.1D7.2B3, Asc# 2761. PSCA is a single subunit glycoprotein that is
 CC expressed on the cell surface as a glycosylphosphatidylinositol (GPI)-
 CC anchored protein. The present invention relates to anti-PSCA antibody
 CC composition and methods of killing PSCA-expressing cancer cells. PSCA is
 CC useful for inhibiting and killing the growth of PSCA-expressing cancer
 CC cells such as prostate cancer, bladder cancer or lung cancer cells.
 CC Humanised antibody conjugated to a toxin or a radioactive isotope is used
 CC for killing the cancer cells. PSCA is useful for specifically targetting
 CC PSCA-expressing tumour cells in vivo and for inhibiting or killing these
 CC cells. The antibodies are also useful for treating the above mentioned
 CC cancers and for diagnosing and staging of PSCA-expressing cancer, for
 CC purification or immunoprecipitation of PSCA from cells, and for detection
 CC and quantitation of PSCA in vitro. PSCA DNA is also useful for treating
 CC cancers by gene therapy techniques
 XX
 SQ Sequence 113 AA;

Query Match 82.5%; Score 571; DB 4; Length 113;
 Best Local Similarity 97.3%; Pred. No. 3.7e-44;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 |||
 Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSTLDS 61
 Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
 |||:||||:|||||
 Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 112

RESULT 14

AAE03756

ID AAE03756 standard; protein; 218 AA.

XX

AC AAE03756;

XX

DT 11-SEP-2003 (revised)

DT 07-AUG-2001 (first entry)

XX

DE Chimeric antibody 6B8 Fab light chain (6B8.1D7.2B3).

XX

KW Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
 KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
 KW human; antibody binding fragment; Fab; light chain region.

XX

OS Mus musculus.

OS Homo sapiens.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 1. .113

FT /note= "Derived from mouse light chain variable region
 FT (VL)"
 FT Region 114. .218
 FT /note= "Derived from human kappa light chain constant
 FT region (Ckappa)"
 XX
 PN WO200140309-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 27-OCT-2000; 2000WO-US029603.
 XX
 PR 29-OCT-1999; 99US-0162558P.
 PR 16-FEB-2000; 2000US-0182872P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Devaux B, Keller G, Koeppen H, Lasky LA;
 XX
 DR WPI; 2001-389954/41.
 XX
 PT Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
 PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-
 PT expressing cancer cells in vivo, useful for killing PSCA-expressing
 PT cancer cells.
 XX
 PS Claim 5; Fig 13; 112pp; English.
 XX
 CC The present chimeric sequence is full length 2761 antibody binding
 CC fragment (Fab) light chain (6B8.1D7.2B3) derived from murine light chain
 CC variable region (VL) and human kappa light chain constant region. This
 CC antibody binds to prostate stem cell antigen (PSCA) which is a single
 CC subunit glycoprotein that is expressed on the cell surface as a
 CC glycosylphosphatidylinositol (GPI)-anchored protein. The present
 CC invention relates to anti-PSCA antibody composition and methods of
 CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
 CC killing the growth of PSCA-expressing cancer cells such as prostate
 CC cancer, bladder cancer or lung cancer cells. Humanised antibody
 CC conjugated to a toxin or a radioactive isotope is used for killing the
 CC cancer cells. PSCA is useful for specifically targetting PSCA-expressing
 CC tumour cells in vivo and for inhibiting or killing these cells. The
 CC antibodies are also useful for treating the above mentioned cancers and
 CC for diagnosing and staging of PSCA-expressing cancer, for purification or
 CC immunoprecipitation of PSCA from cells, and for detection and
 CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
 CC cancers by gene therapy techniques. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 218 AA;

Query Match 82.5%; Score 571; DB 4; Length 218;
 Best Local Similarity 97.3%; Pred. No. 7.8e-44;
 Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 |||
 Db 2 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSTLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||:|||||:|||||
 Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK 112

RESULT 15

AA06273

ID AA06273 standard; protein; 353 AA.

XX

AC AA06273;

XX

DT 23-AUG-1999 (first entry)

XX

DE Anti Fc alpha receptor scFv A77-PDGR-R TM fusion.

XX

KW Single chain antibody; scFv; A77; IgA receptor; Fc receptor;

KW Fc alpha receptor; platelet derived growth factor receptor;

KW antibody engineering; cell surface expression; therapy; cancer; tumour;

KW vaccine; human.

XX

OS Mus sp.

OS Synthetic.

OS Chimeric.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Domain	1. .21
----	--------	--------

FT		/note= "Ig K-chain SP"
----	--	------------------------

FT	Peptide	22. .30
----	---------	---------

FT		/note= "HA epitope"
----	--	---------------------

FT	Domain	38. .160
----	--------	----------

FT		/note= "A77 VL"
----	--	-----------------

FT	Peptide	161. .175
----	---------	-----------

FT		/note= "linker"
----	--	-----------------

FT	Domain	176. .287
----	--------	-----------

FT		/note= "A77 VH"
----	--	-----------------

FT	Peptide	294. .303
----	---------	-----------

FT		/note= "Myc epitope"
----	--	----------------------

FT	Domain	304. .353
----	--------	-----------

FT		/note= "PDGFR transmembrane domain"
----	--	-------------------------------------

XX

PN WO9928349-A2.

XX

PD 10-JUN-1999.

XX

PF 02-DEC-1998; 98WO-US025556.

XX

PR 02-DEC-1997; 97US-0067232P.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Keler T, Goldstein J, Graziano R, Deo YM;

XX

DR WPI; 1999-371099/31.

DR N-PSDB; AAX58936.

XX

PT Cells expressing anti-Fc receptor binding components.

XX
PS Example 6; Fig 10A-E; 68pp; English.

XX
CC The present sequence represents a fusion protein comprising murine anti-
CC Fc alpha receptor antibody A77 sFv and the transmembrane domain of
CC platelet derived growth factor receptor (PDGR-R TM). It is encoded by
CC expression vector pJG718 (see AAX58935). Murine tumour cells transformed
CC to express A77-TM were able to bind a soluble form of the Fc alpha
CC receptor, and the bound receptor was able to engage IgA molecules. This
CC is an example of cells of the invention that have been transformed to
CC express on their surface a component which binds to an Fc receptor of an
CC effector cell. The transformed cell is targeted to an effector cell via
CC the Fc binding component, and can be used as a vehicle to increase an
CC effector cell-mediated immune response, such as cell lysis and
CC phagocytosis, against an antigen associated with the cell. The
CC transformed cells are used to treat cancer and infectious diseases or
CC used as vaccines. The method allows for killing of target cells without
CC targeting any particular antigen on the cell. This is advantageous since
CC many tumour cells and other target cells do not have defined antigens for
CC targeting

XX
SQ Sequence 353 AA;

Query Match 81.2%; Score 562; DB 2; Length 353;
Best Local Similarity 94.6%; Pred. No. 8.7e-43;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
|||||||:|||||||
Db 177 VVMTQTPLTSLITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPTRLIYLVSKLDS 236

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 132
|||||||:|||||:|||||
Db 237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 287

Search completed: May 17, 2004, 11:30:33
Job time : 52.3556 secs

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:29:03 ; Search time 16.1333 Seconds
(without alignments)
422.394 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	649	93.8	131	4	US-09-647-468-163	Sequence 163, App
2	646	93.4	131	4	US-09-647-468-164	Sequence 164, App
3	562	81.2	353	4	US-09-203-958A-4	Sequence 4, Appli
4	560	80.9	112	4	US-09-809-739-11	Sequence 11, Appl
5	559	80.8	112	4	US-09-647-468-149	Sequence 149, App
6	559	80.8	112	4	US-09-647-468-150	Sequence 150, App
7	548	79.2	112	2	US-08-678-194-6	Sequence 6, Appli
8	548	79.2	112	3	US-08-890-011-6	Sequence 6, Appli
9	548	79.2	112	4	US-09-262-724-6	Sequence 6, Appli
10	548	79.2	535	4	US-08-983-035A-38	Sequence 38, Appl
11	538	77.7	112	4	US-09-809-739-16	Sequence 16, Appl

12	537	77.6	132	1	US-08-477-877B-91	Sequence 91, Appl
13	537	77.6	132	2	US-08-472-281A-91	Sequence 91, Appl
14	537	77.6	132	2	US-08-477-989B-91	Sequence 91, Appl
15	533	77.0	112	4	US-09-809-739-17	Sequence 17, Appl
16	530	76.6	112	4	US-09-809-739-15	Sequence 15, Appl
17	525	75.9	112	4	US-09-809-739-18	Sequence 18, Appl
18	520	75.1	112	4	US-09-809-739-14	Sequence 14, Appl
19	518	74.9	132	1	US-08-477-877B-84	Sequence 84, Appl
20	518	74.9	132	2	US-08-472-281A-84	Sequence 84, Appl
21	518	74.9	132	2	US-08-477-989B-84	Sequence 84, Appl
22	515	74.4	135	1	US-08-259-372A-12	Sequence 12, Appl
23	515	74.4	135	1	US-08-468-671-12	Sequence 12, Appl
24	512	74.0	112	3	US-09-184-658-49	Sequence 49, Appl
25	512	74.0	112	4	US-09-504-262D-49	Sequence 49, Appl
26	508	73.4	289	3	US-09-184-658-63	Sequence 63, Appl
27	508	73.4	289	4	US-09-504-262D-63	Sequence 63, Appl
28	504	72.8	113	3	US-09-214-095D-116	Sequence 116, App
29	504	72.8	242	4	US-09-479-614-20	Sequence 20, Appl
30	493.5	71.3	114	2	US-08-672-345C-9	Sequence 9, Appli
31	493.5	71.3	114	3	US-09-214-095D-9	Sequence 9, Appli
32	485	70.1	115	2	US-08-672-345C-99	Sequence 99, Appl
33	468	67.6	112	1	US-08-477-877B-89	Sequence 89, Appl
34	468	67.6	112	2	US-08-472-281A-89	Sequence 89, Appl
35	468	67.6	112	2	US-08-477-989B-89	Sequence 89, Appl
36	466	67.3	111	4	US-09-809-739-13	Sequence 13, Appl
37	465	67.2	112	1	US-08-477-877B-88	Sequence 88, Appl
38	465	67.2	112	2	US-08-472-281A-88	Sequence 88, Appl
39	465	67.2	112	2	US-08-477-989B-88	Sequence 88, Appl
40	463	66.9	131	1	US-08-129-930B-95	Sequence 95, Appl
41	463	66.9	131	3	US-08-134-346A-50	Sequence 50, Appl
42	463	66.9	131	4	US-08-976-288A-95	Sequence 95, Appl
43	461	66.6	112	1	US-07-942-245-28	Sequence 28, Appl
44	458	66.2	149	4	US-09-192-838B-2	Sequence 2, Appli
45	458	66.2	149	4	US-09-324-191-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-647-468-163

; Sequence 163, Application US/09647468

; Patent No. 6677436

; GENERAL INFORMATION:

; APPLICANT: SATO, KOH

; APPLICANT: ADACHI, HIDEKI

; APPLICANT: YABUTA, NAOHIRO

; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

; FILE REFERENCE: 053466/0289

; CURRENT APPLICATION NUMBER: US/09/647,468

; CURRENT FILING DATE: 2000-09-29

; PRIOR APPLICATION NUMBER: PCT/JP99/01768

; PRIOR FILING DATE: 1999-04-02

; PRIOR APPLICATION NUMBER: JP 10-91850

; PRIOR FILING DATE: 1998-04-03

; NUMBER OF SEQ ID NOS: 183

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163
```

```
Query Match          93.8%; Score 649; DB 4; Length 131;
Best Local Similarity 93.9%; Pred. No. 4.1e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLWIREINGDVVLTQTPLTSLVTIGQPASVSCKSSQSLLDSDGKTYLNWL 60

Qy      62 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFTHFPR 121
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 TFGGGTKLEIK 131
```

RESULT 2

```
US-09-647-468-164
; Sequence 164, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164
```

Query Match 93.4%; Score 646; DB 4; Length 131;
Best Local Similarity 93.1%; Pred. No. 7.9e-55;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy      2 MSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWL 61
          |||||: || ||:|||||:|||||:|||||:|||||
Db      1 MSPAQFLFLLVLWIRDINGDVLTQTPLTSLVTIGQPASVSCKSSQSLLDSDGKTYLNWL 60

Qy      62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPR 121
          |||||:|||||:|||||:|||||
Db      61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy      122 TFGGGTKLEIK 132
          |||||
Db      121 TFGGGTKLEIK 131
```

RESULT 3

US-09-203-958A-4

; Sequence 4, Application US/09203958A

; Patent No. 6682928

; GENERAL INFORMATION:

; APPLICANT: KELER, Tibor

; APPLICANT: GOLDSTEIN, Joel

; APPLICANT: GRAZIANO, Robert

; APPLICANT: DEO, Yashwant M.

; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR

; TITLE OF INVENTION: BINDING COMPONENTS

; FILE REFERENCE: MXI-099CPA

; CURRENT APPLICATION NUMBER: US/09/203,958A

; CURRENT FILING DATE: 1998-12-02

; PRIOR APPLICATION NUMBER: 60/067232

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 353

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic construct

US-09-203-958A-4

Query Match 81.2%; Score 562; DB 4; Length 353;
Best Local Similarity 94.6%; Pred. No. 2.8e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:|||||:|||||:|||||
Db      177 VVMTQTPLTSLITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 236

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRFTFGGGTKLEIK 132
          |||||:|||||:|||||
Db      237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFTFGGGTKLEIK 287
```

RESULT 4


```

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

```

```

Query Match          80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGQSPKRLIYLVSKLDS 81
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      2 VVLTQTPLTLSVTIGQPASVSCKSSQSLDSDGKTYLNWLLQRPQGQSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDFTFGGGTKLEIK 112

```

RESULT 6

```

US-09-647-468-150
; Sequence 150, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse

```

; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
||:|||||:|||||
Db 2 VVLTQTPLTSLSVTIGQPASVSCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK 112

RESULT 7

US-08-678-194-6

; Sequence 6, Application US/08678194

; Patent No. 5922845

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; APPLICANT: Graziano, Robert

; APPLICANT: Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor
Antibodi

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; PRIOR APPLICATION DATA: No. 5922845e

; APPLICATION NUMBER: US

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-678-194-6

Query Match 79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.7e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
: :||:||||:|||||||||||||||||||||||||||||||||||||
Db 2 IQLTQSPLTSLITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
||||||||||||||||||:|||||:||||| ||:||||||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

RESULT 8

US-08-890-011-6

; Sequence 6, Application US/08890011
; Patent No. 6193966
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-Fc
; TITLE OF INVENTION: {SYMBOL 97 \f "Symbol"} Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,011
; FILING DATE: July 9, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane E. Remillard
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-011-6

Query Match 79.2%; Score 548; DB 3; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.7e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
: :||:|||||:|||||||||||||||||||||||||||||||||||||
Db 2 IQLTQSPLTSLITIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPTRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
||||||||||||||||||:|||||:||||| |||:|||||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

RESULT 9

US-09-262-724-6

; Sequence 6, Application US/09262724

; Patent No. 6303755

; GENERAL INFORMATION:

; APPLICANT: Deo, Yashwant M.

; Graziano, Robert

; Keler, Tibor

; TITLE OF INVENTION: Therapeutic Multispecific Compounds

; Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"}

; Receptor Antibodies

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/262,724

; FILING DATE: 04-Mar-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/678,194

; FILING DATE: July 11, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Beth A. Arnold

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MXI-064

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

```

;           LENGTH: 112 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-262-724-6

```

```

Query Match          79.2%;  Score 548;  DB 4;  Length 112;
Best Local Similarity 91.0%;  Pred. No. 1.7e-45;
Matches 101;  Conservative 7;  Mismatches 3;  Indels 0;  Gaps 0;

```

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
        : :||:||||:|||||||||||||||||||||||||||||||||||||
Db      2 IQLTQSPLTSLITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPTRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
        ||||||||||||||||:|||||:||||| |||:|||||||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFPQTFGGGTKLEIK 112

```

RESULT 10

US-08-983-035A-38

; Sequence 38, Application US/08983035A
; Patent No. 6326464

; GENERAL INFORMATION:

; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT

; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP

; STREET: 1300 I Street, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/983,035A

; FILING DATE: 20-Feb-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR96/01111

; FILING DATE: 17-JUL-1996

; APPLICATION NUMBER: FR 95/08729

; FILING DATE: 19-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Strauss, William L.

; REGISTRATION NUMBER: 47,114

; REFERENCE/DOCKET NUMBER: 03804.0142

; TELECOMMUNICATION INFORMATION:

```

;          TELEPHONE: 202-408-4000
;          TELEFAX: 202-408-4400
;  INFORMATION FOR SEQ ID NO: 38:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 535 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

```

```

Query Match          79.2%;  Score 548;  DB 4;  Length 535;
Best Local Similarity 92.8%;  Pred. No. 1e-44;
Matches 103;  Conservative 5;  Mismatches 3;  Indels 0;  Gaps 0;

```

```

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      135 VLMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 194

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          |||||:|||||:|||||:|||||:|||||:| ||| |||||:|
Db      195 GVPDRFTGSGSGTDFTLKINRVEAEDLGVYYCWQGTHSPLTFGAGTKLELK 245

```

RESULT 11

US-09-809-739-16

```

; Sequence 16, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
;  APPLICANT: Horvath, Christopher J.
;  APPLICANT: Rao, Patricia E.
;  TITLE OF INVENTION: Method of Inhibiting Stenosis and
;  TITLE OF INVENTION: Restenosis
;  FILE REFERENCE: 1855.1069-003
;  CURRENT APPLICATION NUMBER: US/09/809,739
;  CURRENT FILING DATE: 2001-03-15
;  PRIOR APPLICATION NUMBER: US 09/528,267
;  PRIOR FILING DATE: 2000-03-17
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 16
;  LENGTH: 112
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Humanized sequence
US-09-809-739-16

```

```

Query Match          77.7%;  Score 538;  DB 4;  Length 112;
Best Local Similarity 89.2%;  Pred. No. 1.5e-44;
Matches 99;  Conservative 10;  Mismatches 2;  Indels 0;  Gaps 0;

```

```

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||:||:| ||:|||||||||||||||||||||:|||||||||:|||||
Db      2  VVMTQSPLSLPVTLGQPASISCKSSQSLDSDGKTFLNWLLQRPQGSPRRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132

```

|||||:|||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHTFPYTFGGGTRLEIK 112

RESULT 12

US-08-477-877B-91

; Sequence 91, Application US/08477877B

; Patent No. 5730979

; GENERAL INFORMATION:

; APPLICANT: Bazin, Herv

; APPLICANT: Latinne, Dominique

; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activati

; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi, Stewart & Olstein

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,877B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/407,009

; FILING DATE: 29-MAR-1995

; APPLICATION NUMBER: 08/119,032

; FILING DATE: 09-SEP-1993

; APPLICATION NUMBER: 08/027,008

; FILING DATE: 05-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Olstein, Elliot M.

; REGISTRATION NUMBER: 24,025

; REFERENCE/DOCKET NUMBER: 61750-146

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 91:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 132 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: polypeptide

; FEATURE:

; NAME/KEY: Humanized LO-CD2a light chain variable region.

US-08-477-877B-91

Query Match

77.6%; Score 537; DB 1; Length 132;

Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        |||| | ||||:||| ||| ||||:| :| ||:|||||||:||||| | | |||||
Db      1 MMSPVQSLFLLLLWILGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLHSSGNTYLNW 60

Qy      61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
        |||||||||: ||||||||:||||||:||||||||||| :|||:|:||| | ||:|
Db      61 LLQRPGQSPQPLIYLVSKLESQVPDRFSGSGSGTDFTLKISGVEAEDVGYYCMQFTHYP 120

Qy      121 RTFGGGTKLEIK 132
        ||| |||||
Db      121 YTFGQGTKLEIK 132
```

RESULT 13

US-08-472-281A-91

; Sequence 91, Application US/08472281A

; Patent No. 5817311

; GENERAL INFORMATION:

; APPLICANT: Bazin, Herv

; APPLICANT: Latinne, Dominique

; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activation

; NUMBER OF SEQUENCES: 96

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi, Stewart & Olstein

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,281A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/407,009

; FILING DATE: 29-MAR-1995

; APPLICATION NUMBER: 08/119,032

; FILING DATE: 09-SEP-1993

; APPLICATION NUMBER: 08/027,008

; FILING DATE: 05-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Olstein, Elliot M.

; REGISTRATION NUMBER: 24,025

; REFERENCE/DOCKET NUMBER: 61750-142

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744


```
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 132 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
;   NAME/KEY: Humanized LO-CD2a light chain variable region.
US-08-472-281A-91
```

```
Query Match          77.6%; Score 537; DB 2; Length 132;
Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;
```

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        |||| | ||||:|| | || ||||:| :| ||:|||||||:|||| | | ||||
Db      1 MMSPVQSLFLLLLWILGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLLHSSGNTYLNW 60

Qy      61 LLQRPQGQSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLG LYCWQGTHFP 120
        ||||| ||||: ||||| |||||: ||||| ||||| ||||| ||||| ||||| |||||
Db      61 LLQRPQGQSPQPLIYLVSKLESGVPDRFSGSGSGTDFTLKISGVEAEDVG VYYCMQFTHYP 120

Qy      121 RTFGGGTKLEIK 132
        ||| |||||
Db      121 YTFGQGTKLEIK 132
```

RESULT 14

US-08-477-989B-91

; Sequence 91, Application US/08477989B

; Patent No. 5951983

; GENERAL INFORMATION:

```
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
```

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain
; NAME/KEY: variable region.
US-08-477-989B-91

```

```

Query Match          77.6%; Score 537; DB 2; Length 132;
Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
      |||| | ||||:||| ||| |||||:| :| ||:|||||||:||||| | | |||||
Db      1 MMSPVQSLFLLLLWILGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLLHSSGNTYLNW 60

Qy      61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
      ||||| ||||: ||||| ||||: ||||| ||||| ||||| ||||| ||||| |||||
Db      61 LLQRPGQSPQPLIYLVSKLESGVPDRFSGSGSGTDFTLKISGVEAEDVGYYCMQFTHYP 120

Qy      121 RTFGGGTKLEIK 132
      ||| |||||
Db      121 YTFGQGTKLEIK 132

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RESULT 15

US-09-809-739-17

```

; Sequence 17, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003

```

; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-17

Query Match 77.0%; Score 533; DB 4; Length 112;
Best Local Similarity 88.3%; Pred. No. 4.6e-44;
Matches 98; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy	22	VVMTQTPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS	81
		: : : : : :	
Db	2	VVMTQSPLSLPVTLGHPASISCKSSQSLDSDGKTFLNWLLQRPQGSPRRLIYLVSKLDS	61
Qy	82	GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTFPRTFGGGTKLEIK	132
		: : : : :	
Db	62	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTTFPYTFGGGTRLEIK	112

Search completed: May 17, 2004, 11:33:54
Job time : 17.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.2 Seconds
 (without alignments)
 961.915 Million cell updates/sec

Title: US-10-010-942B-2
 Perfect score: 692
 Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	678	98.0	132	2	C32513	Ig kappa chain pre
2	587	84.8	131	2	S31577	Ig kappa chain - m
3	566	81.8	113	2	F30560	Ig kappa chain V r
4	554	80.1	112	2	A55491	proteolytic antibo
5	548	79.2	112	2	A36259	ig kappa chain V r
6	547	79.0	111	2	S20709	Ig kappa chain V r
7	536	77.5	112	2	PL0273	Ig kappa chain V r
8	516	74.6	133	2	S42611	HUNVK protein prec
9	515	74.4	101	2	A33730	Ig kappa chain V r
10	515	74.4	133	2	S23230	Ig kappa chain pre
11	513	74.1	142	2	S22902	Ig kappa chain V r
12	512	74.0	133	2	S40324	Ig kappa chain V r
13	508	73.4	133	1	K2HURP	Ig kappa chain pre

14	502.5	72.6	140	2	S22658	Ig kappa chain pre
15	496	71.7	133	1	A24452	Ig kappa chain pre
16	491	71.0	132	2	S40322	Ig kappa chain - h
17	485	70.1	103	2	PH1055	Ig light chain V r
18	476	68.8	91	2	S42186	Ig kappa chain V r
19	473	68.4	120	2	S42267	Ig kappa chain V r
20	473	68.4	120	2	S42268	Ig kappa chain V r
21	470	67.9	131	2	S09259	Ig kappa chain pre
22	466	67.3	103	2	PH1056	Ig light chain V r
23	463	66.9	126	2	S40312	Ig kappa chain - h
24	463	66.9	131	2	D29380	Ig kappa chain pre
25	462.5	66.8	131	2	S40355	Ig kappa chain - h
26	462	66.8	132	2	S26882	Ig kappa chain V r
27	461.5	66.7	114	2	S49572	Ig kappa chain pre
28	460	66.5	118	2	S40374	Ig kappa chain - h
29	458.5	66.3	114	2	B49002	Ig kappa chain V r
30	458	66.2	131	2	B34904	Ig kappa chain pre
31	458	66.2	136	2	S40357	Ig kappa chain V-J
32	456	65.9	112	2	A31807	Ig kappa chain V r
33	456	65.9	131	2	B39276	Ig light chain pre
34	455	65.8	132	2	PH0106	anti-digoxin trans
35	454	65.6	131	2	C34904	Ig kappa chain pre
36	452.5	65.4	134	2	S40376	Ig kappa chain - h
37	452	65.3	122	2	S40338	Ig kappa chain - h
38	451	65.2	128	2	S40373	Ig kappa chain - h
39	450.5	65.1	130	2	S40321	Ig kappa chain - h
40	450	65.0	131	2	D34904	Ig kappa chain pre
41	450	65.0	131	2	B30577	Ig kappa chain pre
42	448	64.7	131	2	G34903	Ig kappa chain pre
43	448	64.7	135	2	S40342	Ig kappa chain - h
44	447	64.6	131	2	B32513	Ig kappa chain pre
45	446	64.5	115	2	S38715	Ig kappa chain V r

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C;Accession: C32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.;

Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: C32513

A;Molecule type: DNA

A;Residues: 1-132 <KOF>

A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 678; DB 2; Length 132;
 Best Local Similarity 97.7%; Pred. No. 8.5e-52;
 Matches 129; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLW 60
          |||
Db      1 MMSPAQFLFLLVLWIRETNGDVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |||
Db     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120

Qy    121 RTFGGGTKLEIK 132
          |||
Db    121 RTFGGGTKLEIK 132
  
```

RESULT 2

S31577

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S31577

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antidioxin monoclonals.

A;Reference number: S31577

A;Accession: S31577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-131 <REC>

A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 587; DB 2; Length 131;
 Best Local Similarity 86.3%; Pred. No. 6.3e-44;
 Matches 113; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```

Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLW 61
          |||
Db      1 MSPAQFLFLLVLSIQEINGDVVMQTAPLTLSTIGQPASISCKSSHLLSIDGKTYLW 60

Qy     62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
          |||
Db     61 LQRPQGSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLRISRVEAEDLGVYYCMQNTHTFPY 120

Qy    122 TFGGGTKLEIK 132
          |||
Db    121 TFGGGTKLEMK 131
  
```

RESULT 3

F30560

Ig kappa chain V region (28.4.10A) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
 C;Accession: F30560
 R;Matsuda, T.; Kabat, E.A.
 J. Immunol. 142, 863-870, 1989
 A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.
 A;Reference number: A30560; MUID:89110062; PMID:2464028
 A;Accession: F30560
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-113 <MAT>
 A;Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 566; DB 2; Length 113;
 Best Local Similarity 96.4%; Pred. No. 3.5e-42;
 Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||
Db       2 VVMTQIPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          |||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPHTFGGGTKLEIK 112
  
```

RESULT 4

A55491

proteolytic antibody light chain - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 21-Jan-2000
 C;Accession: A55491
 R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.J.; Paul, S.
 J. Biol. Chem. 269, 32389-32393, 1994
 A;Title: Molecular cloning of a proteolytic antibody light chain.
 A;Reference number: A55491; MUID:95096089; PMID:7798238
 A;Accession: A55491
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-112 <GAO>
 A;Cross-references: GB:L34775
 A;Note: authors translated the codon TAT for residue 37 as Thr
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 554; DB 2; Length 112;
 Best Local Similarity 94.6%; Pred. No. 3.8e-41;
 Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
  
```

```

Db      2  ||||| : |||||
VVM TQTPLT LSVTIGQPASISCKSSQSL LHTDGKTYLIWLLQRP GQSPKRLIYLVSKLDS 61

QY      82  GVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
        ||||| : ||||| : |||||
Db      62  GVPDRFTGSGSGTDFTLKISRVEAEDLG VYYCWQGTHFPQTFGGGTKLEIK 112

```

A36259

C; Species: *Mus musculus* (house mouse)

C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000

C;Accession: A36259

R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.

Biochemistry 29, 10032-10041, 1990

A;Title: NMR-derived model for a peptide-antibody complex.

A;Reference number: A36259; MUID:91104915; PMID:2271636

A;Accession: A36259

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-112 <ZIL>

A;Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482;

GB:M30483

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 548; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.3e-40;
Matches 105; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 2 VVMIQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Db 62 GVPTRFTGSGSGTDFTLKISRVEAEDGQVYYCWQGTHFPWTFGGGTKLEIK 112

S20709

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C;Accession: S20709

R:Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr,

R; Brennand, D.M.; Hinds, M.G.; Welsh, S.R.; Tompkins, R.N.; F.J.; Osborn, N.J.; Glennie, M.J.; Richards, N.G.; Robinson, J.A.

submitted to the EMBL Data Library, April 1992

A;Description: Binding specificity and variable region sequences of two monoclonal antibodies that recognise a beta-turn forming peptide containing alpha-methylproline.

A; Reference number: S20706

A;Accession: S20709

A:Status: preliminary

A;Molecule type: DNA

A;Residues: 1-111 <BRE>
A;Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 547; DB 2; Length 111;
Best Local Similarity 92.7%; Pred. No. 1.5e-40;
Matches 102; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          : ||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db      2  IQLTQSPLTSLVTIGQPASISCKSSQSLHSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEI 131
          ||||||||||||||||||||:|||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHTFPQTFGGGTKLEI 111
```

RESULT 7

PL0273

Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

C;Accession: PL0273

R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-
Rothstein, A.; Weigert, M.

J. Exp. Med. 171, 265-297, 1990

A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and
somatic mutation.

A;Reference number: PL0231; MUID:90111618; PMID:2104919

A;Accession: PL0273

A;Molecule type: mRNA

A;Residues: 1-112 <SHL>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-23/Region: framework 1

F;16-95/Domain: immunoglobulin homology <IMM>

F;24-39/Region: complementarity-determining 1

F;40-54/Region: framework 2

F;55-61/Region: complementarity-determining 2

F;62-93/Region: framework 3

F;94-102/Region: complementarity-determining 3

F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 1.4e-39;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2  VVMTQTPLTSLVTIGQPASISCKSSQSLLYRNGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTFGGGTKLEIK 132
          ||||||||||||||||||||:|||||:|||||:|||||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHTFPWTFGGGTKLEIK 112
```

RESULT 8

S42611

HUNVK protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S42611

R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of two IgM, monoclonal, anti-myelin associated glycoprotein antibodies.

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42611

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <SPA>

A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 516; DB 2; Length 133;
Best Local Similarity 74.0%; Pred. No. 8.8e-38;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

```

QY      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MRLPAQLLGLLMLWVPVGSQSDVVMQTSPLSLPVTLGQPASISCRSSQSLVFSQDNTYLNW 60

QY     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTTHFP 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQGAHWP 120

QY    121 RTFGGGTKLEI 131
      | | | | | | | |
Db    121 LTFGGGTKVEI 131

```

RESULT 9

A33730

Ig kappa chain V region (1.60) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000

C;Accession: A33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlike genes encoding heavy chains, use variable gene segments dispersed throughout the locus.

A;Reference number: A33730; MUID:89367325; PMID:2505260

A;Accession: A33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <LAW>

A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110

A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue 88 as Phe

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

```
Query Match          74.4%;  Score 515;  DB 2;  Length 101;
Best Local Similarity 98.0%;  Pred. No. 8.1e-38;
Matches    97;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
      |||
Db      2 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 61

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
      |||
Db      62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTTHFP 100
```

RESULT 10

S23230

Ig kappa chain precursor V-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S23230

R;Kennedy, M.A.

J. Exp. Med. 173, 1033-1036, 1991

A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light chain V genes in a human B lymphoblastoid cell line.

A;Reference number: S23230; MUID:91178438; PMID:1840606

A;Accession: S23230

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <KEN>

A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

```
Query Match          74.4%;  Score 515;  DB 2;  Length 133;
Best Local Similarity 74.2%;  Pred. No. 1.1e-37;
Matches    98;  Conservative   16;  Mismatches   18;  Indels    0;  Gaps    0;

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
      | ||| | ||:|: :|| ||||:|:| ||:|||||:||||: ||| |:|
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMQTQSPSLPVTLGQPASISCRSSQSLVYSDGNTHLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
      |||||:|||| || |||||:|||||:|||||:||||:| |||:|
Db      61 FQRPQGSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVIYCMQGTTHWP 120

Qy      121 RTFGGGTKLEIK 132
      ||| |||||
Db      121 YTFGQGTKLEIK 132
```

RESULT 11

S22902

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S22902

R;Chastagner, P.; Theze, J.; Zouali, M.

Gene 101, 305-306, 1991

A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region using the polymerase chain reaction and degenerate primers.

A;Reference number: S22902; MUID:91276289; PMID:1905262

A;Accession: S22902

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-142 <CHA>

A;Cross-references: EMBL:X56510

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 1.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
          ||| ||| |||: |||: ||| ||| |||: ||| ||| |||: ||| ||| |||
Db      12 MRLPAQLLGLLMLWVPGSSGDVVMQTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

Qy      61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
          ||| ||| |||: ||| ||| ||| |||: ||| ||| |||: ||| ||| |||: |||
Db      72 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHTWP 131

Qy      121 RTFGGGTKLEI 131
          ||| |||: |||
Db      132 FTFGQGTTRLEI 142
```

RESULT 12

S40324

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40324

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40324

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-133 <KLE>

A;Cross-references: EMBL:X72434

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;
Best Local Similarity 74.4%; Pred. No. 2e-37;

Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

```
Qy      4 PAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQ 63
      ||| | ||:|:| :| ||:|:|:| ||:| ||||| |||: ||||| |||
Db      1 PAQLLGLLMLWVPGSSGDVVLTSPLSLPVTLGQPASISCRSDQSLVYSDGKTYLNWYQQ 60

Qy      64 RPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTFPRTF 123
      |||||:|||| || ||||| ||||| |||||:||||:||||: |||: |||
Db      61 RPGQSPRRLIYKVSNRDSGVPDRFTGSGSGTDFTLEISRVEAEDVGVYYCMQGTHTWPGTF 120

Qy      124 GGGTKLEIK 132
      | |||:|
Db      121 GQGTKVEIK 129
```

RESULT 13

K2HURP

Ig kappa chain precursor V-II region (RPMI) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997

C;Accession: A01890

R;Klobeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.

Nucleic Acids Res. 13, 6499-6513, 1985

A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.

A;Reference number: A93588; MUID:86041852; PMID:2997711

A;Accession: A01890

A;Molecule type: DNA

A;Residues: 1-133 <KLO>

A;Note: the sequence was determined from the differentiated gene

C;Genetics:

A;Gene: GDB:IGKV2

A;Cross-references: GDB:136265

A;Map position: 2p12-2p12

A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>

F;21-43/Region: framework 1

F;36-115/Domain: immunoglobulin homology <IMM>

F;44-59/Region: complementarity-determining 1

F;60-74/Region: framework 2

F;75-81/Region: complementarity-determining 2

F;82-113/Region: framework 3

F;114-122/Region: complementarity-determining 3

F;123-133/Region: framework 4

F;43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;

Best Local Similarity 73.5%; Pred. No. 4.3e-37;

Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
```

```

      | | | | | | | | | | : | | : : | | | | | | | | | | : | | | | | | | | | |
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
      | | | | | | | | | | : | | | | | | | | | | : | | | | | | | | | |
Db      61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120

Qy      121 RTFGGGTKLEIK 132
      | | | | | | | | | |
Db      121 WTFGQGTKVEIK 132

```

RESULT 14

S22658

Ig kappa chain precursor V region (0-81VL) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jan-2000

C;Accession: S22658

R;Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22658

A;Molecule type: mRNA

A;Residues: 1-140 <HIR>

A;Cross-references: EMBL:X59135

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

```

Query Match          72.6%; Score 502.5; DB 2; Length 140;
Best Local Similarity 73.7%; Pred. No. 1.4e-36;
Matches 98; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

```

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
      | | | | | | | | | | : | | : : | | | | | | | | | | : | | | | | |
Db      1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHF- 119
      | | | | | | | | | | : | | | | | | | | | | : | | | | | | | | | |
Db      61 FQQRPGQSPRRLIYRVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQHTHWS 120

Qy      120 PRTFGGGTKLEIK 132
      | | | | | | | | | |
Db      121 PITFGQGTRLEIK 133

```

RESULT 15

A24452

Ig kappa chain precursor V-II region (RPMI 6410) - human

C;Species: Homo sapiens (man)

C;Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999

C;Accession: A24452

R;Weir, L.; Leder, P.

Nucleic Acids Res. 14, 3957-3970, 1986

A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.

A;Reference number: A24452; MUID:86232631; PMID:3086847

A;Accession: A24452

A;Molecule type: DNA

A;Residues: 1-133 <WEI>

A;Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933

A;Note: this sequence was determined from the differentiated gene

C;Genetics:

A;Gene: GDB:IGKV2

A;Cross-references: GDB:136265

A;Map position: 2p12-2p12

A;Introns: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-133/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

F;43-113/Disulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;

Best Local Similarity 72.7%; Pred. No. 4.7e-36;

Matches 96; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

```
QY      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MRLPAQLLGLLRLWVPGSSGDVVMQTSPSLPVTLCQPASISCRSSQSLVYSDRNTYLNW 60

QY     61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGT HFP 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGT HWS 120

QY    121 RTFGGGTKLEIK 132
      | | | | | | | |
Db    121 WTFGQGTKVEIK 132
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Search completed: May 17, 2004, 11:33:08

Job time : 13.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:32:34 ; Search time 37.6444 Seconds
(without alignments)
975.722 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	692	100.0	132	14	US-10-010-942B-2	Sequence 2, Appli
2	692	100.0	132	16	US-10-388-389-2	Sequence 2, Appli
3	650	93.9	135	9	US-09-881-823-10	Sequence 10, Appl
4	649	93.8	131	12	US-10-462-062-163	Sequence 163, App
5	646	93.4	131	12	US-10-462-062-164	Sequence 164, App
6	640	92.5	132	14	US-10-010-942B-5	Sequence 5, Appli
7	640	92.5	132	16	US-10-388-389-5	Sequence 5, Appli
8	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appl
9	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appl
10	630	91.0	132	16	US-10-388-389-11	Sequence 11, Appl
11	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
12	560	80.9	112	9	US-09-835-087-1	Sequence 1, Appli
13	560	80.9	112	9	US-09-809-739-11	Sequence 11, Appl
14	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
15	560	80.9	122	12	US-10-272-899A-86	Sequence 86, Appl
16	560	80.9	130	12	US-10-272-899A-88	Sequence 88, Appl
17	559	80.8	112	12	US-10-462-062-149	Sequence 149, App
18	559	80.8	112	12	US-10-462-062-150	Sequence 150, App
19	556	80.3	112	9	US-09-840-459-54	Sequence 54, Appl
20	551	79.6	500	14	US-10-168-809-22	Sequence 22, Appl
21	548	79.2	112	9	US-09-772-120-6	Sequence 6, Appli
22	548	79.2	535	9	US-09-968-851-38	Sequence 38, Appl
23	547	79.0	162	15	US-10-410-907A-30	Sequence 30, Appl
24	546	78.9	112	15	US-10-323-903-1	Sequence 1, Appli
25	538	77.7	112	9	US-09-835-087-5	Sequence 5, Appli
26	538	77.7	112	9	US-09-809-739-16	Sequence 16, Appl
27	538	77.7	112	9	US-09-840-459-14	Sequence 14, Appl
28	533	77.0	112	9	US-09-835-087-6	Sequence 6, Appli
29	533	77.0	112	9	US-09-809-739-17	Sequence 17, Appl
30	533	77.0	112	9	US-09-840-459-15	Sequence 15, Appl
31	530	76.6	112	9	US-09-835-087-4	Sequence 4, Appli
32	530	76.6	112	9	US-09-809-739-15	Sequence 15, Appl
33	530	76.6	112	9	US-09-840-459-13	Sequence 13, Appl
34	527	76.2	114	9	US-09-840-459-106	Sequence 106, App
35	526	76.0	112	13	US-10-032-482-8	Sequence 8, Appli
36	525	75.9	112	9	US-09-835-087-7	Sequence 7, Appli
37	525	75.9	112	9	US-09-809-739-18	Sequence 18, Appl
38	525	75.9	112	9	US-09-840-459-107	Sequence 107, App
39	520	75.1	112	9	US-09-835-087-3	Sequence 3, Appli
40	520	75.1	112	9	US-09-809-739-14	Sequence 14, Appl
41	520	75.1	112	9	US-09-840-459-12	Sequence 12, Appl
42	515	74.4	100	9	US-09-840-459-22	Sequence 22, Appl
43	511	73.8	132	15	US-10-309-764-117	Sequence 117, App
44	510	73.7	132	15	US-10-309-764-113	Sequence 113, App
45	506	73.1	132	15	US-10-309-764-109	Sequence 109, App

ALIGNMENTS

RESULT 1

US-10-010-942B-2

; Sequence 2, Application US/10010942B

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Guriq

```
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2
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```
Query Match          100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.1e-59;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLSVTIGQPASISCKSSQSLDSDGKTYLNW 60

QY     61 LLQRPQGSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFP 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LLQRPQGSPKRLIYLVS KLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFP 120

QY    121 RTFGGGTKLEIK 132
          |||||||||
Db    121 RTFGGGTKLEIK 132
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RESULT 2

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US-10-388-389-2
; Sequence 2, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
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;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(20)
US-10-388-389-2

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Query Match      100.0%;   Score 692;   DB 16;   Length 132;
Best Local Similarity 100.0%;   Pred. No. 4.1e-59;
Matches 132;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;
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Qy	1	MMSPAQFLFLLVLWIRETNGYVVM	TQTPLT	SVTIGQPASISCKSSQSL	LDSDGKTYLNW	60
Db	1	MMSPAQFLFLLVLWIRETNGYVVM	TQTPLT	SVTIGQPASISCKSSQSL	LDSDGKTYLNW	60
Qy	61	LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDF	TLKISRIE	AEDLGLYYCWQ	GTHFP	120
Db	61	LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDF	TLKISRIE	AEDLGLYYCWQ	GTHFP	120
Qy	121	RTFGGGTKLEIK	132			
Db	121	RTFGGGTKLEIK	132			

Db 1 MMSPAQFLFLLVLWIRETNGYVVM TQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60

QY 61 LLQRPGQSPKRLIYLVS KLDSGV PDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFP 120
 | | | | | | | | | | | | | | | | | | | | | | | | | |

Dh 61 LLORPGOSP KRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120

QY 121 RTFGGGTKLEIK 132
 |||||

Db 121 RTFGGGTKLEIK 132

RESULT 3

US-09-881-823-10

; Sequence 10, Application US/09881823

: Patent No. US20020068066A1

; GENERAL INFORMATION:

; APPLICANT: SHI, WENYUAN

APPLICANT: ANDERSON, MAXWELL

: APPLICANT: MORRISON, SHERIE

; APPLICANT: TRINH, RYAN

; APPLICANT: WIMS, LETITIA

: APPLICANT: CHEN, LI

; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries

FILE REFERENCE: 22851-032

CURRENT APPLICATION NUMBER: US/09/881,823

: CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: US 07/378,577

: PRIOR FILING DATE: 1999-08-20

: NUMBER OF SEO ID NOS: 32

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; SOFTWARE: PatentIn version 3.0

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; SEO ID NO 10

; LENGTH: 135

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; TYPE: PRT

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; ORGANISM: Murine

US-09-881-823-10

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Query Match          93.9%;  Score 650;  DB 9;  Length 135;
Best Local Similarity 93.2%;  Pred. No. 4.7e-55;
Matches 123;  Conservative 5;  Mismatches 4;  Indels 0;  Gaps 0;
```

Matches 123; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSGKTYLNW 60
        ||||||||||||||||| ||||||||||||||||||||| ||: ||:|
Db      1 MMSPAQFLFLLVLWIRETNGDVVMQTPLTSLVTIGQPASISCKSSQSLLDRDGRTYLSW 60
```

Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLDRDGR TYLSW 60

Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 |||:|:|
 Db 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
 |||:|
 Db 121 LTFGAGTKLELK 132

RESULT 4

US-10-462-062-163

; Sequence 163, Application US/10462062
 ; Publication No. US20040044187A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SATO, KOH
 ; APPLICANT: ADACHI, HIDEKI
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
 ; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
 ; FILE REFERENCE: 053466-0360
 ; CURRENT APPLICATION NUMBER: US/10/462,062
 ; CURRENT FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: PCT/JP99/01768
 ; PRIOR FILING DATE: 1999-04-02
 ; PRIOR APPLICATION NUMBER: JP 10-91850
 ; PRIOR FILING DATE: 1998-04-03
 ; NUMBER OF SEQ ID NOS: 183
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 163
 ; LENGTH: 131
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
 ; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
 ; OTHER INFORMATION: antibody ATR-7
 US-10-462-062-163

Query Match 93.8%; Score 649; DB 12; Length 131;
 Best Local Similarity 93.9%; Pred. No. 5.7e-55;
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWL 61
 |||:|:|
 Db 1 MSPAQFLFLLVLWIREINGDVLTQTPLTSLVTIGQPASVSKSSQSLLSDGKTYLNWL 60

Qy 62 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
 |||:|:|
 Db 61 LQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy 122 TFGGGTKLEIK 132
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 Db 121 TFGGGTKLEIK 131

RESULT 5


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; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(20)
;   OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5
```

```
Query Match          92.5%;   Score 640;   DB 14;   Length 132;
Best Local Similarity 90.2%;   Pred. No. 4.3e-54;
Matches 119;   Conservative 10;   Mismatches 3;   Indels 0;   Gaps 0;
```

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLDSDGKTYLNW 60
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MMSPAQFLFLLVLWIRETNGYVVMQSPSLPVTGPGEPAISCKSSQSLDSDGKTYLNW 60

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTTHFP 120
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVIYCWQGTTHFP 120

Qy      121 RTFGGGTKLEIK 132
          |||| |||:|||
Db      121 RTFGQGTKVEIK 132
```

RESULT 7

```
US-10-388-389-5
; Sequence 5, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 132
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: SIGNAL
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RESULT 9

US-10-010-942B-11

```

; Sequence 11, Application US/10010942B

```

; Publication No. US20030165496A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

10 TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

: TITLE OF INVENTION: BETA AMYLOID PEPTIDE

FILE REFERENCE: ELN-002

: CURRENT APPLICATION NUMBER: US/10/010,942B

: CURRENT FILING DATE: 2002-12-06

: PRIOR APPLICATION NUMBER: US 60/251,892

: PRIOR FILING DATE: 2000-12-06

: NUMBER OF SEO ID NOS: 63

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: SOFTWARE: FastSEO for Windows Version 4.0

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: SEO ID NO 11

; LENGTH: 132

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; TYPE: PRT

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: ORGANISM: Artificial Sequence

: FEATURE:

: NAME/KEY: SIGNAL

; LOCATION: (1) . . . (20)

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: OTHER INFORMATION: humanized 3D6 light chain variable region

```

US-10-010-942B-11

Query Match 91.0%; Score 630; DB 14; Length 132;

Best Local Similarity 89.4%; Pred. No. 3.9e-53;

Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTSVTIGQPASISCKSSQSLLDSGKTYLNW 60

27

Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTGPGEPAISCKSSQSLLDSDGKTYLNW 60

Qy 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFP 120

27	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	
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Db 61 LLOKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Cv 121 RTFGGGTKLEIK 132

7-1

||| ||| : |||

Db 121 RTFGQGTKVEIK 132

RESULT 10

US-10-388-389-11

; Sequence 11, Application US/10388389

Publication No. US20040087777A1

; GENERAL INFORMATION:

; APPLICANT: Basi, Gurig

; APPLICANT: Saldanha, Jose

; APPLICANT: Yednock, Ted

: TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

: TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

: FILE REFERENCE: ELN-002CP


```
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 102
;   LENGTH: 142
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-840-459-102
```

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Qy      10 LLVLWIRETNGYVVMQTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNLQRPQGSP 69
      |||
Db      7 LLVLWIRETIGDVVMTQTQTPLTLSVTVGH PASISCKSSQSLDSDGKTFLNWLQRPQGSP 66
      |||

Qy      70 KR LIYLVSKLDSGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGT HFPRTFGGGTKL 129
      |||
Db      67 KR LIYLVSKLDSGVPDRFTGSGSGTDFTLKISR VEAEDLGVYYCWQGT HFPYTFGGGTKL 126
      |||

Qy      130 EIK 132
      |||
Db      127 EIK 129

```

RESULT 12

```
; Sequence 1, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
US-09-835-087-1
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Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81

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Db          2 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQGSPKRLIYLVSKLDS 61
QY          82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db          62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112

```

RESULT 13

US-09-809-739-11

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; Sequence 11, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse

```

US-09-809-739-11

```

Query Match          80.9%; Score 560; DB 9; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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```

QY          22 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQGSPKRLIYLVSKLDS 81
Db          2 VVMTQTPLTSLVTVGHPASISCKSSQSLDSDGKTFLNWLLQRPQGSPKRLIYLVSKLDS 61
QY          82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db          62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKLEIK 112

```


OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.8 Seconds
(without alignments)
961.915 Million cell updates/sec

Title: US-10-010-942B-4
Perfect score: 719
Sequence: 1 MNFGLSLIFLVLVLKGVQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%				
No.	Score	Query	Match	Length	ID	Description
1	573	79.7	138	2	S09258	Ig heavy chain V r
2	569	79.1	152	2	B26471	Ig heavy chain pre
3	559.5	77.8	139	2	S38808	Ig heavy chain - m
4	544	75.7	142	2	C34903	Ig heavy chain pre
5	521.5	72.5	140	2	S70442	Ig heavy chain pre
6	517	71.9	140	2	S31686	Ig heavy chain V r
7	516	71.8	160	2	S05271	Ig heavy chain pre
8	514	71.5	134	2	S31699	Ig heavy chain V r
9	513	71.3	140	2	S31588	Ig heavy chain V r
10	512	71.2	117	1	HVMS84	Ig heavy chain pre
11	510	70.9	117	1	HVMS34	Ig heavy chain pre
12	508	70.7	136	2	S31615	hypothetical prote
13	504	70.1	140	2	S22657	Ig heavy chain pre

14	502.5	69.9	136	1	G1MS21	Ig heavy chain pre
15	502	69.8	138	2	S31666	Ig heavy chain V r
16	501	69.7	117	1	HVMS39	Ig heavy chain pre
17	495	68.8	135	2	S31598	Ig heavy chain V r
18	493	68.6	134	2	S31679	Ig heavy chain V r
19	492.5	68.5	141	2	S31669	Ig heavy chain V r
20	492	68.4	117	1	HVMSRF	Ig heavy chain pre
21	492	68.4	139	2	I37781	Ig variable region
22	490	68.2	122	2	E27888	Ig heavy chain V r
23	487.5	67.8	119	2	F27888	Ig heavy chain V r
24	485.5	67.5	136	2	S31587	Ig heavy chain V r
25	484.5	67.4	151	2	A60943	Ig heavy chain pre
26	484	67.3	117	1	HVMS57	Ig heavy chain pre
27	484	67.3	140	2	A30532	Ig heavy chain pre
28	483	67.2	120	2	S55536	Ig heavy chain V r
29	481.5	67.0	147	2	I37780	Ig variable region
30	480.5	66.8	118	2	PH0096	Ig heavy chain V r
31	480.5	66.8	121	2	S55540	Ig heavy chain V r
32	480.5	66.8	254	2	B31790	Ig heavy chain V r
33	479	66.6	120	2	S55538	Ig heavy chain V r
34	479	66.6	120	2	S55539	Ig heavy chain V r
35	477.5	66.4	121	2	H27888	Ig heavy chain V r
36	477.5	66.4	137	2	S31701	Ig heavy chain V r
37	477.5	66.4	139	2	S31674	Ig heavy chain V r
38	476.5	66.3	137	2	S78054	Ig heavy chain pre
39	476	66.2	120	2	S55537	Ig heavy chain V r
40	473.5	65.9	118	2	PH0097	Ig heavy chain V r
41	472	65.6	132	2	S31603	Ig heavy chain V r
42	471	65.5	130	2	PL0098	Ig heavy chain pre
43	469	65.2	118	2	S20641	Ig heavy chain V r
44	467.5	65.0	135	2	I37778	Ig variable region
45	467.5	65.0	145	2	S11239	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 573; DB 2; Length 138;
 Best Local Similarity 80.4%; Pred. No. 1.4e-42;
 Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGLSLIFLVLILKGVQCEVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy     61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
          :|||||:| |||| ||| |:||||| |:||| ||||| |:||||| ||
Db     61 EKRLEWVATISSGGGNTYYPDVSKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

Qy    121 YSGSSDYWGQGTTVTVSS 138
          |      ||||| ||||:
Db    121 YEAWFASWGQGLTVTVSA 138
  
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RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C;Accession: B26471; S70410

R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987

A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a
 creatine-kinase-specific monoclonal antibody.

A;Reference number: A91572; MUID:87248058; PMID:3110009

A;Accession: B26471

A;Molecule type: mRNA

A;Residues: 1-152 <BUC>

A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406

R;Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 172, 1717-1727, 1990

A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5'
 boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.

A;Reference number: S70410; MUID:91079775; PMID:2258702

A;Accession: S70410

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-19 <LEB>

A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;
 Best Local Similarity 78.2%; Pred. No. 3.5e-42;
 Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

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Qy      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          |||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
  
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Db          1 MNFGLSLIFLVLVLKGVQCEVQGVESGGGLVKPGGSLKLSCAASGFTFSDYYMYWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
              :|||||||:|  ||  |||  |:|||||||:||||  |||||:|||||
Db          61 EKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDKA 120
Qy          118 -YDHYSGSSDYWGQGTTVTVSS 138
              | :|  : |||||:|||||
Db          121 YYGNYGDAMDYWGQGTSTVTVSS 142

```

RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000

C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

```

Query Match          77.8%;  Score 559.5;  DB 2;  Length 139;
Best Local Similarity 79.3%;  Pred. No. 2.1e-41;
Matches 111;  Conservative 8;  Mismatches 16;  Indels 5;  Gaps 2;

```

```

Qy          1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          1 MNFGFSLIFLVLVLKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTP 60
Qy          61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
              :||||||| ||  ||  |||  |:|||||||:|:|  |||||:||||:|  |
Db          61 EKRLEWVASI-SRGGTTYYPDSVKGRFTISRDNARNNLYLQMSSLRSEDAMYYCAREGI 119
Qy          121 YSG----SSDYWGQGTTVTV 136
              ||  ||  |||||:|||
Db          120 YGYALYGMDYWGQGTSTVTV 139

```

RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive anti-fluorescein monoclonal antibodies.

A;Reference number: A34903; MUID:90094387; PMID:2104617

A;Accession: C34903

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-142 <BED>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 544; DB 2; Length 142;
Best Local Similarity 76.1%; Pred. No. 4.7e-40;
Matches 108; Conservative 9; Mismatches 21; Indels 4; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 MNFGFSLIFLVVLKGVQCEVKWVESGGGLVSPGGSLKLSCAASGFTFSTYAMSWVRQTP 60

Qy     61 DKRLEWVASI--RSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRY 118
        :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     61 EKRLEWVASFGNKPTGGRTYYPDVSVKGRFTISRDNARNILYLQMSSLRSEDTAMYYCARG 120

Qy    119 DHYSGS--SDYWGGQTTVTVSS 138
        :| | ||||| ||||| :
Db    121 GYYYGGYWFAFWGQGTTLTVSA 142
```

RESULT 5

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000

C;Accession: S70442

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnel, C.

Mol. Immunol. 29, 1363-1373, 1992

A;Title: IgM kappa/lambda EBV human B cell clone: an early step of differentiation of fetal B cells or a distinct B lineage?

A;Reference number: S70442; MUID:93024508; PMID:1383695

A;Accession: S70442

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 72.5%; Score 521.5; DB 2; Length 140;
Best Local Similarity 71.4%; Pred. No. 4.1e-38;
Matches 100; Conservative 18; Mismatches 19; Indels 3; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
        | ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      1 MEFGLSWVFLVALLRGVQCQVQLVESGGGVVQPGGSLRLSCAASGFTFSNYGMHWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
        | ||| | | | :||| :||| :||| :||| :||| :||| :||| :|||
```

Db 61 GKGLEWVAFIRYDGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAR-DH 119

Qy 121 YSGSS--DYWGQGTTVTVSS 138
 |:: ||||| |||||

Db 120 IVGATYFDYWGQGTTLVTVSS 139

RESULT 6

S31686

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31686

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31686

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 517; DB 2; Length 140;
 Best Local Similarity 70.7%; Pred. No. 9.9e-38;
 Matches 99; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | ||| : || : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

Db 1 MEFGLSWLSLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGRTYYSDNVKGRFTISRDN SKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | ||| : || || ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

Db 61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKCPF 120

Qy 121 YSGSS--DYWGQGTTVTVSS 138
 || ||||| |||||

Db 121 AGGSPSFDYWGQGTTLVTVSS 140

RESULT 7

S05271

Ig heavy chain precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996

C;Accession: S05271; S04602

R;Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A;Reference number: S05270

A;Accession: S05271

A;Molecule type: mRNA

A;Residues: 1-160 <KIS1>

A;Cross-references: EMBL:X14584

R;Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A;Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.

A;Reference number: S04601; MUID:89296497; PMID:2500644

A;Accession: S04602

A;Molecule type: mRNA

A;Residues: 1-144 <KIS2>

A;Cross-references: EMBL:X14584

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 516; DB 2; Length 160;

Best Local Similarity 68.1%; Pred. No. 1.4e-37;

Matches 98; Conservative 18; Mismatches 22; Indels 6; Gaps 1;

```
QY      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

QY     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
      | | | | : : | | | | | | | | | | | | | | | | | | | | | | :
Db     61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKAVV 120

QY    118 ---YDHYSGSSDYWGQGTTTVTVSS 138
      : | | | | | | | | | |
Db    121 RGVISYYYYGMDVWGQGTTTVTVSS 144
```

RESULT 3

S31699

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31699

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver.

A;Reference number: S31585

A;Accession: S31699

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <CUI>

A;Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 514; DB 2; Length 134;

Best Local Similarity 71.0%; Pred. No. 1.7e-37;

Matches 98; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | | | | : | | : | | | | | : | : | | | | | | | : | | | | |
 Db 1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVHPGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | | | | : : | | | | : | | | | | : | : | | | | | : | : | | | : | | :
 Db 61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARW-- 118

Qy 121 YSGSSDYWGQGT TVTVSS 138
 | | | | | | | | | |
 Db 119 --RDL DYWGQGT LVTVSS 134

RESULT 9

S31588

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31588

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
 submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
 from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31588

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-140 <CUI>

A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 513; DB 2; Length 140;
 Best Local Similarity 69.3%; Pred. No. 2.2e-37;
 Matches 97; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 | | | | : | | : | | | | | : | : | | | | | | | : | | | | |
 Db 1 MEFGLSWLFLVAILRGVQCEVQLLES GGGLVQPGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 | | | | : : | | | | : | | | | | : | : | | | | | : | : | | | : | | :
 Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKDHD 120

Qy 121 YSG--SSDYWGQGT TVTVSS 138
 | | | | | | | | | |
 Db 121 YSNYIYFDYWGQGT LVTVSS 140

RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C;Accession: JT0505

R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

```
F;41-115/Disulfide bonds: #status predicted
```

F;41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 510; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 3.3e-37;
Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
||| | | | | | | | | | : | | | : | | | | | | | | | | | | : | | | | |
Db 1 MNFGLRLIFLVLTCLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSSYDMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
: | | | | | | | | | | | | | | | : | | | | | | | | | | | | : | | | |
Db 61 EKRLEWVAYISSGGGSTYYPDTVKGRFTISRDNKNTLYLOMSSLKSEDTAMYYCAR 117

RESULT 12

S31615

hypothetical protein - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text change 23-Jul-1999

C;Accession: S31615

R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, April 1991

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidioxin monoclonal.

A;Reference number: S31615

A;Accession: S31615

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <REC>

A;Cross-references: EMBL:X58884; NID:g51824; PIDN:CAA41688.1; PID:g51825

C; Superfamily: immunoglobulin V region; immunoglobulin homology

T;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 508; DB 2; Length 136;

Best Local Similarity 70.3%; Pred. No. 5.8e-37;

Matches 97; Conservative 16; Mismatches 23; Indels 2; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      ||||| ||||| |||||:| ||||| ||||| :|||:| ||| | ||||
Db      1 MNFGLRLIFLVLTCLKGVQCDVNLVESGGGLVKPGGTLKLSCSASGFAFSTYSMVWVRQTP 60

Qy      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      :|||:| || || |:|:| |||||:| |:| |||:| |:|:|
Db      61 EKRLEWVATITGGGTYTYYPDSVRGRFTISRDNARDTLNLHMTNLKSEDTAMYYCLGYW 120

Qy      121 YSGSSDYWGQGTTVTVSS 138
      | |: ||||| | |:
Db      121 YDGT--YWGOGTLVIVSA 136

```

RESULT 13

S22657

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C; Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence revision 06-Feb-1998 #text change 06-Feb-1998

C;Accession: S22657

R; Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A;Reference number: S22657; MUID:92285150; PMID:1598223

A;Accession: S22657
 A;Molecule type: mRNA
 A;Residues: 1-140 <HIR>
 A;Cross-references: EMBL:X59134
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;
 Best Local Similarity 68.1%; Pred. No. 1.3e-36;
 Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

```

Qy      1 MNFGLSLIFLVLVKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
      | | | | : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEFGLSWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAASGFTFSSHWMTWVRQTP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
      | | | | | | | | : | | | | | | | | | | | | | | | | | | | | |
Db     61 GKRLEWVANVKQDGSARYYADSVRGRFTISRDNAKNSLYLQMDSLRADDTAVYYCAR--- 117

Qy    121 YSGSSDYWGQGTTVTVSS 138
      | | | | | | | | | |
Db    118 -STGIDYWGQGTTLTVSS 134
  
```

RESULT 14

G1MS21

Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999

C;Accession: E90809; A93184; A02066

R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.

Cell 24, 625-637, 1981

A;Title: Heavy chain variable region contribution to the NP(b) family of antibodies: somatic mutation evident in a gamma2a variable region.

A;Reference number: A90809; MUID:81234548; PMID:6788376

A;Accession: E90809

A;Molecule type: mRNA

A;Residues: 1-136 <BOT>

A;Cross-references: GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055

R;Adetugbo, K.; Milstein, C.; Secher, D.S.

Nature 265, 299-304, 1977

A;Title: Molecular analysis of spontaneous somatic mutants.

A;Reference number: A93184; MUID:77100368; PMID:401950

A;Contents: myeloma protein MOPC 21

A;Accession: A93184

A;Molecule type: protein

A;Residues: 17-74, 'D', 76-77, 'H', 79-88, 'ND', 91-114, 'H', 116-119, 'W', 121-136 <ADE>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>

F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>

F;31-114/Domain: immunoglobulin homology <IMM>

F;115-119/Region: D segment

F;120-136/Region: J segment (JH4)
F;38-112/Disulfide bonds: #status experimental

Query Match 69.9%; Score 502.5; DB 1; Length 136;
Best Local Similarity 70.4%; Pred. No. 1.7e-36;
Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

```
Qy      5 LSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
          |:|:|||||:|||||:|:|||||:|:| | |||||:|:| | ||| :| |
Db      2 LNLVFLVLILKGVQCDVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGL 61

Qy     65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYS-G 123
          |||| | || :|:| |||||:| | |||:|:|:|:|:|:| | | :| :|
Db     62 EWVAYISSGSSTLHYADTVKGRFTISRDNPKNLTLFLOMTSLRSEDAMYYCARWGNYPYY 121

Qy    124 SSDYWQGTTVTVSS 138
          : |||||:|||||
Db    122 AMDYWQGTSVTVSS 136
```

RESULT 15

S31666

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31666

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-138 <CUI>

A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 502; DB 2; Length 138;
Best Local Similarity 67.6%; Pred. No. 1.9e-36;
Matches 96; Conservative 21; Mismatches 17; Indels 8; Gaps 2;

```
Qy      1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
          | |||| :||| :|||||:|:|||||:| | ||:|||||:|:| | |||||
Db      1 MEFGLSWLFLVAILKGVQCEVQLLES GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy     61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
          | ||||:| | |||:|:|||||:|:|:|||||:|:|:|||||:| | :
Db     61 GKGLEWVSAISGGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKART 120

Qy    118 -YDHYS GSSDYWGQTTVTVSS 138
          | :| | ||:| | |||||
Db    121 GYWYF----DLWGRGTLVTVSS 138
```

Search completed: May 17, 2004, 11:33:09
Job time : 14.8 secs

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:23:58 ; Search time 34.7111 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description

1	611	88.3	148	11	Q8K122	Q8k122 mus musculu
2	583	84.2	239	11	Q8K0F8	Q8k0f8 mus musculu
3	511	73.8	239	4	Q8TCD0	Q8tcd0 homo sapien
4	471	68.1	239	4	Q8NEK0	Q8nek0 homo sapien
5	460	66.5	238	11	Q99M37	Q99m37 mus musculu
6	459	66.3	238	11	Q8VCI6	Q8vci6 mus musculu
7	453	65.5	239	11	Q8VC55	Q8vc55 mus musculu
8	444.5	64.2	114	4	Q9UL80	Q9ul80 homo sapien
9	398	57.5	104	11	Q9JL82	Q9jl82 mus musculu
10	362.5	52.4	236	11	Q7TS98	Q7ts98 mus musculu
11	348.5	50.4	111	11	Q811U6	Q811u6 mus musculu
12	346	50.0	86	4	Q7Z3Y5	Q7z3y5 homo sapien
13	341.5	49.3	111	11	Q920E9	Q920e9 mus musculu
14	329.5	47.6	234	11	Q8R062	Q8r062 mus musculu
15	323.5	46.7	234	11	Q91WF8	Q91wf8 mus musculu
16	322.5	46.6	234	4	Q7Z473	Q7z473 homo sapien
17	322	46.5	109	4	Q9UL78	Q9ul78 homo sapien
18	321.5	46.5	236	11	Q7TMK3	Q7tmk3 mus musculu
19	315.5	45.6	107	11	Q9ERZ9	Q9erz9 mus musculu
20	313.5	45.3	134	11	Q8VDD0	Q8vdd0 mus musculu
21	313.5	45.3	237	13	Q7SZ36	Q7sz36 xenopus lae
22	311	44.9	107	4	Q96SA9	Q96sa9 homo sapien
23	307.5	44.4	108	11	Q8VIJ0	Q8vij0 mus musculu
24	307.5	44.4	236	4	Q7Z3Y4	Q7z3y4 homo sapien
25	306.5	44.3	214	11	Q9R1A5	Q9rla5 mus musculu
26	305.5	44.1	108	4	Q9UL70	Q9ul70 homo sapien
27	304.5	44.0	108	4	Q9UL79	Q9ul79 homo sapien
28	303.5	43.9	127	11	Q925S9	Q925s9 mus musculu
29	301.5	43.6	108	4	Q9UL77	Q9ul77 homo sapien
30	298.5	43.1	233	11	Q91WS9	Q91ws9 mus musculu
31	296	42.8	112	11	Q8K1F2	Q8k1f2 mus musculu
32	295	42.6	107	4	Q9UL81	Q9ul81 homo sapien
33	295	42.6	114	11	Q8K1F1	Q8k1f1 mus musculu
34	294	42.5	112	11	Q8K1F3	Q8k1f3 mus musculu
35	293.5	42.4	103	11	Q9JL80	Q9jl80 mus musculu
36	292	42.2	106	5	Q9U410	Q9u410 schistosoma
37	291.5	42.1	108	4	Q9UL83	Q9ul83 homo sapien
38	290	41.9	109	4	Q9UL86	Q9ul86 homo sapien
39	289.5	41.8	235	11	Q91W12	Q91w12 mus musculu
40	288.5	41.7	99	11	Q9JL74	Q9jl74 mus musculu
41	288	41.6	109	4	Q9UL85	Q9ul85 homo sapien
42	288	41.6	131	11	Q811C3	Q811c3 mus musculu
43	287.5	41.5	234	11	Q8VCP0	Q8vcp0 mus musculu
44	280.5	40.5	101	11	Q9JL78	Q9jl78 mus musculu
45	279.5	40.4	235	11	Q7TMK0	Q7tmk0 mus musculu

ALIGNMENTS

RESULT 1

Q8K122

ID Q8K122 PRELIMINARY; PRT; 148 AA.

AC Q8K122;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC028925; AAH28925.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 88.3%; Score 611; DB 11; Length 148;
 Best Local Similarity 97.5%; Pred. No. 9.9e-59;
 Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWL 61
 |||||
 Db 1 MSPAQFLFLLVLWIRETNGDVVMQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWL 60
 Qy 62 LQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLG LY YCWQGT HFP 120
 |||||:|||||:|||||
 Db 61 LQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR VEAEDLG VY YCWQGT HFP 119

RESULT 2

Q8K0F8

ID Q8K0F8 PRELIMINARY; PRT; 239 AA.
 AC Q8K0F8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC031498; AAH31498.1; -.
 DR PIR; A33933; A33933.
 DR PDB; 1KN2; 13-MAR-02.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002198; ADH_short.

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 84.2%; Score 583; DB 11; Length 239;
 Best Local Similarity 87.1%; Pred. No. 2.2e-55;
 Matches 115; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 ||||| | :| || ||||| | :|| ||:|
 Db 1 MMSPAQFLFLLVLSIQEINGDVMTQTPLTSLVTIGQPASISCKSSQSLFYTNKGMYLSW 60

 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 ||||| | :||| | :||| | :||| | |||
 Db 61 LLQRPQGSPKRLISLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP 120

 Qy 121 RTFGGGTKLEIK 132
 ||||| |
 Db 121 YTFGGGKLEIK 132

RESULT 3

Q8TCD0

ID Q8TCD0 PRELIMINARY; PRT; 239 AA.
 AC Q8TCD0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC022362; AAH22362.1; -.
 DR PIR; S34095; S34095.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 73.8%; Score 511; DB 4; Length 239;
Best Local Similarity 72.7%; Pred. No. 1.6e-47;
Matches 96; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPTLTLSTIGQPASISCKSSQSLLDSDGKTYLNW 60
| ||| | ||:|: ::| ||||:|:| ||:|||||:|:|: ||| |||||
Db 1 MRLPAQLLGLLMLWVPGSSGDVVMQTSPSLPLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60

Qy 61 LLQRPQGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
|||||:|:| || |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVG VYFCMQGTHWP 120

Qy 121 RTFGGGTKLEIK 132
||| |||||
Db 121 STFGQGTKLEIK 132

RESULT 4

Q8NEK0

ID Q8NEK0 PRELIMINARY; PRT; 239 AA.
AC Q8NEK0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40357; S40357.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 68.1%; Score 471; DB 4; Length 239;

Best Local Similarity 68.2%; Pred. No. 3.8e-43;
Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        | ||| | ||:|: :| :|||:|:| | | |:| |||:| ||| | ||:|
Db      1 MRLPAQLLGLLMLWVSGSGDIVMTQSPLSLPVTGPGEPAISCRSSQSLLHSDGYNLDW 60

Qy     61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
        ||:|||||: ||| | |||||:|||||||:|:|:|:|:|:| | | |
Db     61 YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTP 120

Qy     121 RTFGGGTKLEIK 132
        :||| |||:|
Db     121 QTFGQGTKVEIK 132
```

RESULT 5

Q99M37

```
ID   Q99M37      PRELIMINARY;      PRT;      238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
DR   PIR; A31807; A31807.
DR   PIR; A32248; A32248.
DR   PIR; B32248; B32248.
DR   PIR; C32248; C32248.
DR   PIR; F32530; F32530.
DR   PIR; PH1042; PH1042.
DR   PIR; PH1043; PH1043.
DR   PIR; PH1044; PH1044.
DR   PIR; S07455; S07455.
DR   PIR; S16112; S16112.
DR   PIR; S24500; S24500.
DR   PIR; S24501; S24501.
DR   PIR; S24503; S24503.
DR   PIR; S24504; S24504.
DR   PIR; S24529; S24529.
DR   PIR; S24532; S24532.
DR   PIR; S24533; S24533.
DR   PIR; S24535; S24535.
DR   PIR; S24536; S24536.
DR   PIR; S24538; S24538.
DR   PDB; 1I9I; 25-DEC-02.
DR   PDB; 1LO2; 31-JUL-02.
DR   PDB; 1LO4; 31-JUL-02.
DR   InterPro; IPR007110; Ig-like.
```


DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 66.5%; Score 460; DB 11; Length 238;
 Best Local Similarity 69.6%; Pred. No. 6e-42;
 Matches 87; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Qy 8 LFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQG 67
 | : | : | | : : | | | | | | : | | : | | | | : | | | | | : | |
 Db 7 LLVLMFWIPASSSDVVMQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQ 66
 Qy 68 SPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLG LY YC WQ GTHFPRTFGGGT 127
 | | | | | | | | | | : | | | | | | | | | | : | | | | : | | : | | | |
 Db 67 SPKLLIYKVS NRFS GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQ GSHVPYTFGSGT 126
 Qy 128 KLEIK 132
 | | | |
 Db 127 KLEIK 131

RESULT 6

Q8VCI6

ID Q8VCI6 PRELIMINARY; PRT; 238 AA.
 AC Q8VCI6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC019760; AAH19760.1; -.
 DR PIR; A27887; A27887.
 DR PIR; A32248; A32248.
 DR PIR; A33933; A33933.
 DR PIR; B27887; B27887.
 DR PIR; B30577; B30577.
 DR PIR; B31485; B31485.
 DR PIR; B32248; B32248.
 DR PIR; B41940; B41940.
 DR PIR; C27887; C27887.
 DR PIR; C32248; C32248.
 DR PIR; C34904; C34904.
 DR PIR; D27887; D27887.
 DR PIR; D29380; D29380.

DR PIR; E28833; E28833.
 DR PIR; F32530; F32530.
 DR PIR; H31485; H31485.
 DR PIR; PH0106; PH0106.
 DR PIR; PH1030; PH1030.
 DR PIR; PH1031; PH1031.
 DR PIR; PH1034; PH1034.
 DR PIR; PL0257; PL0257.
 DR PIR; PT0359; PT0359.
 DR PIR; S07455; S07455.
 DR PIR; S16112; S16112.
 DR PIR; S26334; S26334.
 DR PIR; S53750; S53750.
 DR PIR; S60066; S60066.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 66.3%; Score 459; DB 11; Length 238;
 Best Local Similarity 70.4%; Pred. No. 7.7e-42;
 Matches 88; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 8 LFLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPQG 67
 | : | : | | : : | | | | | | : | | : | | | | : | | : | | : | |
 Db 7 LLVLMFWIPASSSDVVMQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ 66

 Qy 68 SPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHFPRTFGGGT 127
 | | | | | | | | | | | | | | | | | | | | | | : | | | | | | | |
 Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPTFGGGT 126

 Qy 128 KLEIK 132
 | | | |
 Db 127 KLEIK 131

RESULT 7

Q8VC55

ID Q8VC55 PRELIMINARY; PRT; 239 AA.
 AC Q8VC55;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC021781; AAH21781.1; -.
 DR PIR; A33933; A33933.
 DR PDB; 1KC5; 24-JUL-02.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR004214; Conotoxin.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF02950; Conotoxin; 1.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 65.5%; Score 453; DB 11; Length 239;
 Best Local Similarity 67.4%; Pred. No. 3.5e-41;
 Matches 89; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 | | : ||: :: ||:||||:| | || |||||:||||:| | ||:|
 Db 1 MKLPVLLVLLLTSPASSSDVLTQTPLSLPVNIGDQASISCKSTKSLNSDGFYLDW 60

 Qy 61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHTP 120
 ||:||||: ||||| |||||:|||||:|||||:||||:| | |
 Db 61 YLQKPGQSPQLLIYLVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLP 120

 Qy 121 RTFGGGTKLEIK 132
 |||||
 Db 121 YTFGGGTKLEIK 132

RESULT 8

Q9UL80

ID Q9UL80 PRELIMINARY; PRT; 114 AA.
 AC Q9UL80;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035034; AAD56270.1; -.
 DR PIR; B49002; B49002.
 DR PIR; S23638; S23638.
 DR PIR; S34094; S34094.
 DR PIR; S34095; S34095.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 64.2%; Score 444.5; DB 4; Length 114;
 Best Local Similarity 76.8%; Pred. No. 1.1e-40;
 Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTSLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 |||||:|:| ||: |||||:|||| : ||| ||||| |||||:|||| || ||
 Db 2 VVMTQSPLSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPQGSPRRLIYKVSNRDS 61
 Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR-TFGGGTKLEIK 132
 |||||:|||||:|||||:||||:| ||| |||:|||
 Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVIYCMQGTHWPPWTFGQGTKVEIK 113

RESULT 9

Q9JL82

ID Q9JL82 PRELIMINARY; PRT; 104 AA.
 AC Q9JL82;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 RT with cardiac myosin."
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206024; AAF69322.1; -.
 DR PIR; S26334; S26334.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.

```
DR    PROSITE; PS50835; IG_LIKE; 1.
FT    NON_TER            1            1
FT    NON_TER           104          104
SQ    SEQUENCE          104 AA;   11360 MW;   5DA8BBFD5F0AA1AE CRC64;
```

```
Qy      29  LTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDSGVPDRFT 88
          |:| |:| |::| |::|:|::|: ::| |::| |::| |::| |::| |::|:
Db      1  LSLPVS LGDQASISCRSSQSLVHTNGNTYLHWYLOKPGQSPKLLIYKVS NREFSGVPDRFS 60
```

RESULT 10

```
ID      Q7TS98      PRELIMINARY;      PRT;      236 AA.
AC      Q7TS98;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Anti-colorectal carcinoma light chain.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93383497; PubMed=8372513;
RA      Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT      "Cloning and characterization of 1116NS19.9 heavy and light chain
RT      cDNAs and expression of antibody fragments in Escherichia coli.";
RL      Year Immunol. 7:56-62(1993).
DR      EMBL; S65921; AAB28160.1; -.
SQ      SEQUENCE      236 AA;  26454 MW;  2C586EBF5EA10F4C CRC64;
```

```

Qy      1 MMSPAQFLFLLVLWIRETINGYVVMQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
        | :| | | | :| :| |      : | | :| :: ::| : :| :| :| |      | :| :|
Db      3 MRTPAQFLGILLLLWFPGMKCDIKMTQSPSSMYASLGERTVITCKASQ-----DINSYLSW 57

```

Qy 121 RTFGGGTKLEIK 132
 |||||
 Db 118 RTFGGGTKLEIK 129

0811U6

```
Query Match          50.4%;  Score 348.5;  DB 11;  Length 111;
Best Local Similarity 58.6%;  Pred. No. 3.4e-30;
Matches    65;  Conservative    19;  Mismatches    26;  Indels      1;  Gaps      1;
```

Qy	22	VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS	81
		: : : : : : : : : ::: :	
Db	1	IVLTQSPASLAVSLGQRATISCKASQS-VDFDGDSEFMNWWYQQKPGQPPKLLIYTTSNLES	59
Qy	82	GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK	132
		: : :	
Db	60	GIPARFSASGSGTDFTLNIHPVEEEDTATYYCOOSNEDPYTFGGGTKLELK	110

Q7Z3Y5

```
ID      Q7Z3Y5          PRELIMINARY;          PRT;          86 AA.
AC      Q7Z3Y5;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Rearranged VKA17 V gene segment (Fragment).
GN      VKA17.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
 RA Hansmann M.L., Brauninger A.;
 RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
 RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
 RT cell precursor in a germinal center."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ564426; CAD92033.1; -.
 FT NON_TER 1 1
 FT NON_TER 86 86
 SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match 50.0%; Score 346; DB 4; Length 86;
 Best Local Similarity 79.7%; Pred. No. 4.6e-30;
 Matches 63; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 42 SCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKIS 101
 ||:||||: ||| |||| | |||||:|||| | | |||||:|||||||
 Db 1 SCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRD SGVPDRFSGSGSGTDFTLKIS 60
 Qy 102 RIEAEDLGLYYCWQGT HFP 120
 |:||||:|:|||| ||||:|
 Db 61 RVEAEDVG VYYCMQGT HWP 79

RESULT 13

Q920E9

ID Q920E9 PRELIMINARY; PRT; 111 AA.
 AC Q920E9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotope kappa chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
 RT in Mammalian Cells."
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF307935; AAL09419.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 49.3%; Score 341.5; DB 11; Length 111;
Best Local Similarity 57.7%; Pred. No. 2e-29;
Matches 64; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

```
Qy      22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
          :|:|:| :|:|:| :|:|:|:|:| : : | :|:| | :| | | | | | :|
Db      2 IVLTQSPASLAVSLGQRATISCRASKS-VSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60

Qy      82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
          ||| ||:||||||| | :| || || | ||||| | |
Db      61 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKLEIK 111
```

RESULT 14

Q8R062

ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

Query Match 47.6%; Score 329.5; DB 11; Length 234;
Best Local Similarity 52.3%; Pred. No. 1.1e-27;
Matches 69; Conservative 17; Mismatches 41; Indels 5; Gaps 1;

```
Qy      1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNW 60
          ||| |||| ||:| :| : |||| :|| :| :||| :|| : |||
Db      1 MMSSAQFLGLLLLCFQGTRCDIQMTQTSSLSASLGDRVTISCSASQGI-----SNYLNW 55

Qy      61 LLQRPQGSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
          |:| : | ||| | | |||| ||:||||| :| || :| ||: ||| | : ||
Db      56 YQQKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDATYYCQQYSQFP 115

Qy      121 RTFGGGTKLEIK 132
          ||| |||||
Db      116 FTFGSGTKLEIK 127
```


RESULT 15

Q91WF8

ID Q91WF8 PRELIMINARY; PRT; 234 AA.
 AC Q91WF8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC015292; AAH15292.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 46.7%; Score 323.5; DB 11; Length 234;
 Best Local Similarity 51.5%; Pred. No. 4.9e-27;
 Matches 68; Conservative 19; Mismatches 40; Indels 5; Gaps 1;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMQTPTLTLVTIGQPASISCKSSQSLLDSDGKTYLNW 60
 ||| |||| ||:| :| : |||| :|| :|| :|||:| | ||||
 Db 1 MMSSAQFLGLLLLCFQGTRCDIQMTQTSSLSASLGDRVTISCRASQ-----DISNYLNW 55
 Qy 61 LLQRPQGSPKRLIYLVSKLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFP 120
 |:| :| ||| |:| ||| ||:|||||||:| || :| ||: |:| || |
 Db 56 YQQKPDGTVKLLIYYTSRLYLGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTTP 115
 Qy 121 RTFGGGTKLEIK 132
 ||| |||||:|
 Db 116 FTFGSGTKLEVK 127

Search completed: May 17, 2004, 11:32:29
 Job time : 35.7111 secs

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:11:13 ; Search time 9.77778 Seconds
 (without alignments)
 702.947 Million cell updates/sec

Title: US-10-010-942B-2
 Perfect score: 692
 Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	508	73.4	133	1	KV2F_HUMAN	P06310	homo sapien
2	434	62.7	113	1	KV2G_MOUSE	P01631	mus musculu
3	417	60.3	117	1	KV2E_HUMAN	P06309	homo sapien
4	415	60.0	113	1	KV2D_HUMAN	P01617	homo sapien
5	414.5	59.9	115	1	KV2A_HUMAN	P01614	homo sapien
6	414	59.8	113	1	KV2B_HUMAN	P01615	homo sapien
7	389.5	56.3	112	1	KV2C_HUMAN	P01616	homo sapien
8	388	56.1	113	1	KV2F_MOUSE	P01630	mus musculu
9	386	55.8	129	1	KV3L_HUMAN	P18135	homo sapien
10	380.5	55.0	134	1	KV4C_HUMAN	P06314	homo sapien
11	380	54.9	113	1	KV2E_MOUSE	P03976	mus musculu
12	374	54.0	112	1	KV2D_MOUSE	P01629	mus musculu
13	374	54.0	120	1	KV2B_MOUSE	P01627	mus musculu
14	373.5	54.0	131	1	KV3I_MOUSE	P01661	mus musculu
15	373	53.9	113	1	KV2C_MOUSE	P01628	mus musculu
16	373	53.9	129	1	KV3M_HUMAN	P18136	homo sapien
17	373	53.9	133	1	KV4B_HUMAN	P06313	homo sapien

18	369	53.3	112	1	KV2A_MOUSE	P01626	mus musculu
19	363.5	52.5	108	1	KV1_CANFA	P01618	canis famil
20	358.5	51.8	111	1	KV3L_MOUSE	P01664	mus musculu
21	358.5	51.8	128	1	KV3K_HUMAN	P06311	homo sapien
22	357	51.6	129	1	KV3H_HUMAN	P04207	homo sapien
23	353.5	51.1	111	1	KV3M_MOUSE	P01665	mus musculu
24	353.5	51.1	111	1	KV3O_MOUSE	P01667	mus musculu
25	352.5	50.9	111	1	KV3N_MOUSE	P01666	mus musculu
26	350.5	50.7	128	1	KV5E_MOUSE	P01637	mus musculu
27	348.5	50.4	111	1	KV3Q_MOUSE	P01669	mus musculu
28	348.5	50.4	111	1	KV3R_MOUSE	P01670	mus musculu
29	347	50.1	110	1	KV3P_MOUSE	P01668	mus musculu
30	343.5	49.6	111	1	KV3J_MOUSE	P01662	mus musculu
31	343.5	49.6	114	1	KV4A_HUMAN	P01625	homo sapien
32	339.5	49.1	111	1	KV3H_MOUSE	P01660	mus musculu
33	337.5	48.8	111	1	KV3U_MOUSE	P01673	mus musculu
34	335.5	48.5	111	1	KV3K_MOUSE	P01663	mus musculu
35	335.5	48.5	111	1	KV3T_MOUSE	P01672	mus musculu
36	335.5	48.5	129	1	KV1W_HUMAN	P04431	homo sapien
37	333.5	48.2	111	1	KV3S_MOUSE	P01671	mus musculu
38	333.5	48.2	132	1	KV3F_MOUSE	P01658	mus musculu
39	333.5	48.2	136	1	KV5B_MOUSE	P01634	mus musculu
40	332.5	48.0	115	1	KV3I_HUMAN	P04433	homo sapien
41	328.5	47.5	108	1	KV5P_MOUSE	P01649	mus musculu
42	328.5	47.5	111	1	KV3C_MOUSE	P01656	mus musculu
43	328.5	47.5	121	1	KV40_HUMAN	P06312	homo sapien
44	325.5	47.0	111	1	KV3A_MOUSE	P01654	mus musculu
45	323.5	46.7	149	1	KV5A_MOUSE	P01633	mus musculu

ALIGNMENTS

RESULT 1

KV2F_HUMAN

ID KV2F_HUMAN STANDARD; PRT; 133 AA.

AC P06310;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region RPMI 6410 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041852; PubMed=2997711;

RA Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;

RT "Human immunoglobulin kappa light chain genes of subgroups II and

RT III.";

RL Nucleic Acids Res. 13:6499-6513(1985).

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OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83178921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 RT anti-digoxin hybridoma antibody.";
 RL Biochemistry 22:1153-1158(1983).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
 CC PROTEIN THAT BINDS DIGOXIN.
 DR PIR; A01914; KVMS26.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 62.7%; Score 434; DB 1; Length 113;
 Best Local Similarity 75.7%; Pred. No. 5.5e-36;
 Matches 84; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 |||||:|:| ||||:||||: |:| ||||| |:| ||||| ||| |||
 Db 2 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRFS 61
 QY 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGFHPRTFGGGTKLEIK 132
 |||||:|||||||:|||||:|:| ||| ||||| |||||
 Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGGTKLEIK 112

RESULT 3

KV2E_HUMAN

ID KV2E_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region GM607 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=84191506; PubMed=6325927;
 RA Klobeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain
 RT diversity.";
 RL Nature 309:73-76(1984).
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 CC -----
 DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 5 27 FRAMEWORK-1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 58 FRAMEWORK-2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 66 97 FRAMEWORK-3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 107 116 FRAMEWORK-4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 60.3%; Score 417; DB 1; Length 117;
 Best Local Similarity 69.6%; Pred. No. 2.7e-34;
 Matches 80; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 18 TNGYVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLV 77
 :| :|||:|:| || |:|||||:||||| |:| ||:| ||:| |||: |||| |
 Db 2 SSGDIVMTQSPLSLPVTGPGEPAISCRSSQSLHLSNGYNYLDWYLQKPQQSPQLLIYLG 61
 Qy 78 KLD SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGFHPRTFGGGTKLEIK 132
 |||||:|||||:|||||:|||||:|:| || |:| |||: |||
 Db 62 NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGYYCMQGLQTPQTFGQGTKVEIK 116

RESULT 4
 KV2D_HUMAN
 ID KV2D_HUMAN STANDARD; PRT; 113 AA.
 AC P01617;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region TEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of
 RT primary amyloidosis.";
 RL Biochemistry 12:3763-3780(1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
 RA Glenner G.G.;
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a
 RT patient with plasma cell dyscrasia and amyloidosis.";
 RL J. Clin. Invest. 52:1276-1281(1973).
 CC -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
 CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
 CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 DR PIR; A90370; K2HUTW.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

 Query Match 60.0%; Score 415; DB 1; Length 113;
 Best Local Similarity 71.2%; Pred. No. 4.1e-34;
 Matches 79; Conservative 14; Mismatches 18; Indels 0; Gaps 0;

QY 22 VVMTQTPLTSLVITIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 :||||:|:| || |:|||||:||||| ||| |||| |:|||||: ||| :| |

Db 2 IVMTQSPSLPVTGPGEPAISCRSSQSLHSDGFDYLNWYLQKPGQSPZLLIYALSNRAS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||:|||||:|||||:|||||:| ||| ||:|||||

Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVIYCMZALQAPITFGQGTREIK 112

RESULT 5

KV2A_HUMAN

ID KV2A_HUMAN STANDARD; PRT; 115 AA.

AC P01614;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region Cum.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=68242259; PubMed=5586923;

RA Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
 RT type).";

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).

RN [2]

RP REVISIONS TO 50; 52; 96 AND 97.

RX MEDLINE=70063440; PubMed=4188189;

RA Hilschmann N.;

RT "Molecular basis of antibody formation.";

RL Naturwissenschaften 56:195-205(1969).

CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; B91639; K2HUCM.

DR HSSP; P01607; 1REI.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 24 95 BY SIMILARITY.

FT NON_TER 115 115

SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 59.9%; Score 414.5; DB 1; Length 115;

Best Local Similarity 72.3%; Pred. No. 4.7e-34;

Matches 81; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTSLVSTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLD 80
 :|||||:| || |:|||||:||||| || ||||| |: ||||: ||| :|

Db 3 IVMTQTPLSLPVTGPGEPAISCRSSQSLDSDGNTYLNWYLQKAGQSPQLLIYTLSTYRA 62

Qy 81 SGVPDRFTGSGSGTDFTLKISR IEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 ||| ||| : ||| ||| ||| ||| : : ||| : | : ||| | | ||| ||| ||| :
Db 63 SGVPDRFSGSGSGTDFTLKISRVQAEDVG VYYCMQRLEIPYTFGQGTKLEIR 114

62 GVPDRFSDSGSGTDFTLKITRVOAEDVGYYCMOATZSPYTFGOGTKLZIK 112

KV2C HUMAN

```
Query Match      56.3%;  Score 389.5;  DB 1;  Length 112;
Best Local Similarity 63.1%;  Pred. No. 1.3e-31;
Matches 70;  Conservative 24;  Mismatches 16;  Indels 1;  Gaps 1;
```

Qy	22	VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS	81
		: : : : : : : : : : : : : : :	
Db	2	IVLTQSPLSLPVTPEGEPASISCRSSQNLLZSBGB-YLDWYLZKPGZSPZLLIYLGSNRAS	60
Qy	82	GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK	132
		: : : : : : : : : :	
Db	61	GVPNRFSGSGSGTBTFTLKISRVAZBVGVIYCMQALQTPITFGGGTNVEIK	111

RESULT 8

Qy 121 RTFGGGTKLEIK 132
 |||| |::|||
 Db 117 RTFGQGTKVEIK 128

RESULT 10

KV4C_HUMAN

ID KV4C_HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 RA Marsh P., Mills F., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe."
 RL Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RP REVISION TO 76.
 RA Marsh P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; X02990; CAA26733.1; -.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 133 FRAMEWORK-4.

FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 54.9%; Score 380; DB 1; Length 113;
 Best Local Similarity 65.8%; Pred. No. 1.2e-30;
 Matches 73; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 :||| : ||:| |||||:|:| ||| ||:||||: |:| :| |
 Db 2 IVMTQAVFSNPVTLGTSASISCRSSKSLHNSGITYLYWYLQKPGQSPQLLLYQMSNLAS 61
 Qy 82 GVPDRFTGSGSGTDFTLTKISRIEADLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||: ||||| ||||:|:| ||| | ||||| |||||
 Db 62 GVPDRFSSSGSGTDFTLRISRVEADVGVYYCAHNLELPYTFGGGTKLEIK 112

RESULT 12

KV2D_MOUSE

ID KV2D_MOUSE STANDARD; PRT; 112 AA.
 AC P01629;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region 2S1.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83055101; PubMed=7141411;
 RA Herbst H., Chang J.Y., Aebersold R., Braun D.G.;
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
 RT the group A streptococcal polysaccharide.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
 CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
 CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR; A01911; KVMSS1.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;

Query Match 54.0%; Score 374; DB 1; Length 112;
 Best Local Similarity 65.8%; Pred. No. 4.5e-30;
 Matches 73; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQGSPKRLIYLVSKLDS 81
 :||| : ||:| || ||:|:| | | ||| | ||:||||: ||| :| | |
 Db 2 IVMTQAAFSNPVTLGTSASFSCRSSKSLQSKGITYLYWYLQKPGQSPQLLIYQMSNLAS 61

Qy 82 GVPDRFTGSGSGTDFTLTKISRIEADLGLYYCWQGTHTFPRTFGGGTKLEIK 132
 |||||:|||||||:||||:|:| | | |||||
 Db 62 GVPDRFSGSGSGTDFTLRISRVEAEDVGVYYCANLQELPYTFGGGTKLEIK 112

RESULT 13

KV2B_MOUSE

ID KV2B_MOUSE STANDARD; PRT; 120 AA.
 AC P01627;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region VKappa167 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82002223; PubMed=6791832;
 RA Selsing E., Storb U.;
 RT "Somatic mutation of immunoglobulin light-chain variable-region
 RT genes.";
 RL Cell 25:47-58(1981).

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DR EMBL; J00562; AAA39032.1; -.
 DR EMBL; K02415; AAA39051.1; -.
 DR PIR; A01909; KVMS67.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 60 74 FRAMEWORK-2.

